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OM protein - protein search, using sw model

Run on: August 28, 2002, 12:23:41 ; Search time 30.25 Seconds
(without alignments)
1721.371 Million cell updates/sec

Title: US-09-522-278b-12
Perfect score: 1561
Sequence: 1 MTSRRSVKSGPPEVRRDEYE.....PTERRAPARCSAPRRPVE 301

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:.*
1: sp_archaea:.*
2: sp_bacteria:.*
3: sp_fungi:.*
4: sp_human:.*
5: sp_invertebrate:.*
6: sp_mammal:.*
7: sp_mhc:.*
8: sp_organelle:.*
9: sp_phage:.*
10: sp_plant:.*
11: sp_rodent:.*
12: sp_virus:.*
13: sp Vertebrate:.*
14: sp_unclassified:.*
15: sp_virus:.*
16: sp_bacteriophage:.*
17: sp_archaeal:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1014.5	65.0	300	12	P89468 herpes simp
2	270.5	17.3	304	12	O39253 equine herp
3	228	14.6	301	12	O9E206 cercopithec
4	210	13.5	249	12	O69318 marek's dis
5	210	13.5	249	12	O96697 turkey herp
6	207	13.3	241	12	O89247 gallid herp
7	198	12.7	283	12	O9DHC2
8	168.5	10.8	388	4	O9NY42
9	168.5	10.8	441	4	O75685
10	153	9.8	252	12	O9DMG9
11	149.5	9.6	956	4	O9UO39
12	149.5	9.6	2752	4	O9UO35
13	149.5	9.6	3122	12	P89459
14	148	9.5	266	12	O56868 gallid herp
15	146.5	9.4	395	16	O9RV74
16	146.5	9.4	1343	4	O9H7N4

17	146	9.4	839	16	O9RX57	O9rx57 delinococcus
18	146	9.4	1262	4	O9UO40	O9u040 homo sapien
19	144	9.2	1037	16	O9AC25	O9ac25 caulobacter
20	144	9.2	1201	10	O9C651	O9c651 arabidopsis
21	143.5	9.2	889	4	O9UL51	O9ul51 homo sapien
22	143.5	9.2	1154	4	O9P2P0	O9p2p0 homo sapien
23	142	9.1	1249	5	O9N8G4	O9n8g4 trypanosoma
24	140.5	9.0	1265	3	O59920	O59920 pneumocysti
25	140.5	9.0	1992	3	O9P6T1	O9p6t1 neurospora
26	140	9.0	1132	16	O9PRC7	O9prc7 delinococcus
27	139.5	8.9	932	5	O93562	O93562 caenorhabdit
28	139	8.9	438	16	O9A2W5	O9a2w5 caulobacter
29	138.5	8.9	1312	4	O9NR59	O9nr59 homo sapien
30	137	8.8	590	2	O9S205	O9s205 streptomyces
31	137	8.8	797	2	O9RKS9	O9rks9 streptomyces
32	137	8.8	835	2	O9K3E2	O9k3e2 streptomyces
33	137	8.8	1069	12	O69140	O69140 human herpe
34	136.5	8.7	694	6	O9GKY7	O9gky7 oryctolagus
35	136.5	8.7	889	4	O9UBS2	O9ub52 homo sapien
36	136.5	8.7	1320	11	O08784	O08784 mus musculu
37	136	8.7	212	11	O70446	O70446 mus musculu
38	136	8.7	436	4	O96S01	O96s01 homo sapien
39	136	8.7	2936	5	O9NKP7	O9nkp7 leishmania
40	135.5	8.7	612	2	O9Z614	O9z614 streptomyces
41	135.5	8.7	1175	6	O9TV66	O9tv66 oryctolagus
42	134	8.6	667	11	O9R1D9	O9r1d9 mus musculu
43	134	8.6	721	4	O96E48	O96e48 homo sapien
44	134	8.6	737	11	O9WVF3	O9wvf3 mus musculu
45	134	8.6	806	11	O9WVF4	O9wvf4 mus musculu

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	300 AA.
1	P89468			
AC	P89468:			
DT	01-MAY-1997 (TREMBLrel. 03, Created)			
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	TEGUMENT PROTEIN.			
GN	UL49.			
OS	Herpes simplex virus (type 2).			
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;			
OX	Alphaherpesvirinae; Simplexvirus.			
NCBI_Taxid=10310;				
[1]	SEQUENCE FROM N.A.			
RP	STRAIN-HG52:			
RC	MEDLINE-87111457; PubMed-3027242;			
RA	McGeoch D.J., Moss H.W., McNab D., Frame M.C.;			
RT	"DNA sequence and genetic content of the HindIII 1 region in the short			
RT	unique component of the herpes simplex virus type 2 genome:			
RT	identification of the gene encoding glycoprotein G, and evolutionary			
RT	comparisons."			
U. Gen. Virol. 68:19-38(1987).				
[2]	SEQUENCE FROM N.A.			
RP	STRAIN-HG52:			
RC	MEDLINE-90278430; PubMed-2161906;			
RX	Everett R., Fenwick M.;			
RA	"Comparative DNA sequence analysis of the host shut-off genes of			
RT	different strains of herpes-simplex virus: type 2 strain HG52 encodes			
RT	a truncated UL41 product."			
U. Gen. Virol. 71:1387-1390(1990).				
[3]	SEQUENCE FROM N.A.			
RP	STRAIN-HG52:			
RC	MEDLINE-92113549; PubMed-1662697;			
RA	McGeoch D.J., Cunningham C., McIntyre G., Dolan A.;			
RT	"Comparative sequence analysis of the long repeat regions and			
RT	adjointing parts of the long unique regions in the genomes of herpes			

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RT simplex viruses types 1 and 2."
RL J. Gen. Virol. 72:3057-3075(1991).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-HG52:
RX MEDLINE-92356101; PubMed-1322965;
RA Bernick B.C., Dolan A., Telford E.A.R., Davison A.J., McGeoch D.J.;
RT "A novel herpes simplex virus gene (UL49A) encodes a putative membrane
RT protein with counterparts in other herpesviruses."
RL J. Gen. Virol. 73:2167-2171(1992).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-HG52:
RA Dolan A.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z86099; CAB06735.1; -.
SQ SEQUENCE 300 AA; 31790 MW; FC72D09F7FB7B096 CRC64;

Query Match 65.0%; Score 1014.5; DB 12; Length 300;
Best Local Similarity 69.2%; Pred. No. 1.3e-62;
Matches 209; Conservative 19; Mismatches 71; Indels 3; Gaps 3;

QY 1 MTSRSVSKSGPREVPREDYEDLYTTPSSGMASSPSPDTSRGAALQTRSRQGEVRFYQ 60
DB 1 MTSRSVSKSGPREVPREDYEDLYTTPSSGMASSPSPDTSRGAALQTRSRQGEVRFYQ 60
QY 61 DESDYALYGGSSSEDDHEHVPRTTRRPVSGAVLSGPPARAPPPAGSGA-GRTPTTAP 119
DB 61 DESDYALYGGSSSEDDHEHVPRTTRRPVSGAVLSGPPARAPPPAGSGA-GRTPTTAP 119
QY 60 DEAGYALYRGSSSDDESRDTRARRRSASVAGSHGPPARAPPPGPGVAGGSHAPRA 119
DB 60 DEAGYALYRGSSSDDESRDTRARRRSASVAGSHGPPARAPPPGPGVAGGSHAPRA 119
QY 120 RAPRTORVATKAPAPAAETTRGRKSAOPESALPDAPASTAPTRSKTPAAGLARKLHFS 179
DB 120 RAPRTORVATKAPAPAAETTRGRKSAOPESALPDAPASTAPTRSKTPAAGLARKLHFS 179
QY 120 RTPKMTGAPKASATPATDPRKGRPAQADSAYLLDAPAPTAAGRTKTPAAGLAKLHFS 179
DB 120 RTPKMTGAPKASATPATDPRKGRPAQADSAYLLDAPAPTAAGRTKTPAAGLAKLHFS 179
QY 180 TAPNPAPAPPTPRVAGFNKRVFCAVGRLAAMHARMAAVQMDMSRRTDDELLELGIT 239
DB 180 TAPNPAPAPPTPRVAGFNKRVFCAVGRLAAMHARMAAVQMDMSRRTDDELLELGIT 239
QY 180 TAPSPAPAPPTPRVAGFNKRVFCAVGRLAATARLAAYQMDMSRPTDDELLELGLT 239
DB 180 TAPSPAPAPPTPRVAGFNKRVFCAVGRLAATARLAAYQMDMSRPTDDELLELGLT 239
QY 240 TIRTVCEKNLQORANELVNDVQDDAATATRGSAASPRPRPARASAPRRP 299
DB 240 TIRTVCEKNLQORANELVNDVQDDAATATRGSAASPRPRPARASAPRRP 299
QY 240 TIRTVCEKNLQORANELVNDVQDDAATATRGSAASPRPRPARASAPRRP 299
DB 240 TIRTVCEKNLQORANELVNDVQDDAATATRGSAASPRPRPARASAPRRP 299
QY 300 VE 301
DB 299 LE 300

RESULT 2
QY 039253 PRELIMINARY; PRT; 304 AA.
AC 039253;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE COUNTERPART OF HSV-1 GENE UL49 AND VZV GENE 9.
GN 11.
OS Equine herpesvirus 4.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10331;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NS80567;
RX MEDLINE-94058670; PubMed-8240007;
RA Riggall M., Onions D.E.;
RT "DNA sequence of a gene cluster in the equine herpesvirus-4 genome
RT which contains a newly identified herpesvirus gene encoding a membrane
RT protein."
RL Arch. Virol. 133:171-178(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-NS80567;

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RX MEDLINE-98264497; PubMed-9603335;
RA Telford E.A., Watson M.S., Perry J., Cullinane A.A., Davison A.J.;
RT "The DNA sequence of equine herpesvirus-4."
RL J. Gen. Virol. 79:1197-1203(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-NS80567;
RA Telford E.A., Watson M.S., Perry J., Cullinane A.A., Davison A.J.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF030027; AAC59525.1; -.
SQ SEQUENCE 304 AA; 33483 MW; 07A8725F7774FC43 CRC64;

Query Match 17.3%; Score 270.5; DB 12; Length 304;
Best Local Similarity 34.4%; Pred. No. 2.4e-11;
Matches 85; Conservative 18; Mismatches 77; Indels 67; Gaps 11;

QY 60 YDES DYALYGGSSSEDDHEHVPRTTRRPVSGAVLSGCG---PARAPPPAGSGAGRTPT 116
DB 98 YDACEYSLVGG-----GKLTSHGRUSPTKTHPK---SAGVTP- 134
QY 117 TAPAPRTORVATKAPAPAAETTRGRKSAOPESALPDAPASTAPTRSKTPAAGL--AR 174
DB 135 -----PQRY-----PARPAT-----RAAP--SATPTQPDCAKQRTSGVNSIRSGK 175
QY 175 KLHSTAPPNPDAPWTBPRVAGFNKRVFCAVGRLAAMHARMAAVQMDMSRPTDDELNE 234
DB 176 SLAFSCPTPKPTKPTWYGATHLFNKNVFCAAVSRVAALHAASDAALMDLDPKPTNEGLDR 235
QY 235 LIGTTIRVYCEKNLQORANELVNDVQDDAATATRRS---AASPTRRPAPA 290
DB 236 FLKAAAIRILVCEKSLLEMAN-----ATMERSPDGAATAVPIGYDRP- 279
QY 291 RSASRPR 297
DB 280 RLASRRR 286

RESULT 3
QY 09E206 PRELIMINARY; PRT; 301 AA.
AC 09E206;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE HYPOHETICAL 33.2 KDA PROTEIN.
OS Cercarial dermatitis virus 7.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=35245;
RN [1]
RP SEQUENCE FROM N.A.
RA Gray W.L., Starnes H.B., White M.W., Ashburn C.V., Mahalingam R.;
RT "Complete sequence of the Simian Varicella Virus Genome."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF275348; AAC27246.1; -.
KW Hypothetical protein.
SQ SEQUENCE 301 AA; 33161 MW; A451C744DC844A02 CRC64;

Query Match 14.6%; Score 228; DB 12; Length 301;
Best Local Similarity 26.1%; Pred. No. 2e-08;
Matches 91; Conservative 26; Mismatches 86; Indels 146; Gaps 14;

QY 4 RRSVSKSGPREVPREDYEDLYTTPSSGMASSPSPDTSRGAALQTRSRQGEVRFYQ 59
DB 39 RRSVAVG---FPDSDSLGIAT---VETSPLEYGDS--GTVDR-----HTMIS 85
QY 60 YDES DYALYGGSSSEDDHEHVPRTTRRPVSGAVLSGCG---PARAPPPAGSGAGRTPT 116
DB 60 YDES DYALYGGSSSEDDHEHVPRTTRRPVSGAVLSGCG---PARAPPPAGSGAGRTPT 116
QY 86 NNSSD-----SDDFEDIDEVIAAFKARLKHENHEDAVENYQHGNAQPMIKN 137
DB 86 NNSSD-----SDDFEDIDEVIAAFKARLKHENHEDAVENYQHGNAQPMIKN 137
QY 86 RVSAGAVLSGPPARAPPPAGSGAGRTPTTAPRAPRTORVATKAPAPAAETTRGRKS 145

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Db 138 RDVD-----SEKRAP-----GAG-----151
Oy 146 ACPESALADAPASTAPTSTKTPAOGKLHSTAPRPNDAWTPRVAGFNKRVCAAV 205
Db 152 -----ALASGRPLSESTAPKNTTSACGPTPAYNKRVCCEAI 188
Oy 206 GRLAAMHAMAAYVOLWDMSPRTDEDLNELGTTTIRVYCEGKNLORANELV---NDP 262
Db 189 RRIIAAQORAAEAAMSSNPNNALDLRLAGTVYRITVHEGLNIQVANDLELGCKPD 248
Oy 263 -----VVQDYDAATATATGRSASRPT-----RRAPASASRP 296
Db 249 RKOSTARRKKEIYKTDDEPYVAQVAKINSRGTPVSGTSRARRRVSXK 297

RESULT 4
Oy 069318 PRELIMINARY; PRT; 249 AA.
AC 069318:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE UL49H.
GN UL49.
OS Marek's disease herpesvirus (strain GA) (MDHV), and
OC Turkey herpesvirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_TaxID=10390;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=galid herpesvirus 1, and Turkey herpesvirus; STRAIN=GA;
RX MEDLINE=93389438; PubMed=8397281;
RA Yanagida N., Yoshida S., Nazerian K., Lee L.F.;
RT "Nucleotide and predicted amino acid sequences of Marek's disease
RT virus homologues of herpes simplex virus major tegument proteins.";
RL J. Gen. Virol. 74:1837-1845(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Turkey herpesvirus; STRAIN=GA;
RX MEDLINE=92237304; PubMed=1315048;
RA Jones D., Lee L., Liu J.L., Kung H.J., Tillotson J.K.;
RT "Marek disease virus encodes a basic-leucine zipper gene resembling
RT the fos/jun oncogenes that is highly expressed in lymphoblastoid
RT tumors.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4042-4046(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Turkey herpesvirus; STRAIN=GA;
RA Lee L.F., Wu P., Sul D., Ren D., Kung H.J.;
RT "The complete UL sequence of Serotype I Marek's disease virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2000).
DR EMBL: L10283; AAA03148.1;
DR EMBL: AF147806; AAF66784.1;
SQ SEQUENCE 249 AA; 27656 MW; B251007B6720F651 CRC64;
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Query Match 13.5%; Score 210; DB 12; Length 249;
Best Local Similarity 25.9%; Pred. No. 2.9e-07;
Matches 74; Conservative 33; Mismatches 93; Indels 86; Gaps 9;

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Oy 38 DTSRRGALOTRSRQREVFYQYDESDYALYGSSSEDDHEPVP-----RTRRVSGA 91
Db 3 DSERRKSERRRS-----LGPSAYDD--VSIARRRSTRTQRLNLD 42
Oy 92 VLSGPGAPARPPPPAGSGAGRTPTTAPRAPRTOR--VATKAPAAPAAETTRGRKSAOPES 150
Db 43 DLSKHGPFTHDP-----TQKHSAKAVSEDSVSTTRGGFTKRP-- 80
Oy 151 AALPDAPASTAPTSTKTPAOGKL-ARKLHSTAPRPNDAWTPRVAGFNKRVCAAVGRLA 209
Db 81 -----RTKPGVRAVOSNKFASFSTAPSSASTWRSNTVAFNORMCGAVATVA 127
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Oy 210 AMHARMAAYVOLWDMSPRTDEDLNELGTTTIRVYCEGKNL-----LQ 253
Db 128 QYHAYGALALMRQDPPRNEELDAFLSRAVYKITTIOEGPNLMGEAETCARKLLESGLS 187
Oy 254 RANELVNPVVDVDAATATRG-----RSAASRPTERRAPARS 292
Db 188 QGNEVKKSKSERTTKSERTTRRGGEIEIKSPDPGSHHTHNPRTATS 233

RESULT 5
Oy 09E6M7 PRELIMINARY; PRT; 249 AA.
AC 09E6M7:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE UL49 TEGUMENT PHOSPHOPROTEIN-LIKE PROTEIN.
GN MDV062.
OS Turkey herpesvirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae.
OX NCBI_TaxID=10390;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MD5;
RX MEDLINE=20392152; PubMed=10933706;
RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
RT "The genome of a very virulent Marek's disease virus.";
RL J. Virol. 74:7980-7988(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MD5;
RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
RT Submitted (MAR-2000) to the EMBL/GenBank/DDO databases.
DR EMBL: AF243438; AAG14242.1;
SQ SEQUENCE 249 AA; 27626 MW; 58F00BCB7631F65D CRC64;
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Query Match 13.5%; Score 210; DB 12; Length 249;
Best Local Similarity 25.9%; Pred. No. 2.9e-07;
Matches 74; Conservative 33; Mismatches 93; Indels 86; Gaps 9;

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Oy 38 DTSRRGALOTRSRQREVFYQYDESDYALYGSSSEDDHEPVP-----RTRRVSGA 91
Db 3 DSERRKSERRRS-----LGPSAYDD--VSIARRRSTRTQRLNLD 42
Oy 92 VLSGPGAPARPPPPAGSGAGRTPTTAPRAPRTOR--VATKAPAAPAAETTRGRKSAOPES 150
Db 43 DLSKHGPFTHDP-----TQKHSAKAVSEDSVSTTRGGFTKRP-- 80
Oy 151 AALPDAPASTAPTSTKTPAOGKL-ARKLHSTAPRPNDAWTPRVAGFNKRVCAAVGRLA 209
Db 81 -----RAKPGVRAVOSNKFASFSTAPSSASTWRSNTVAFNORMCGAVATVA 127
Oy 210 AMHARMAAYVOLWDMSPRTDEDLNELGTTTIRVYCEGKNL-----LQ 253
Db 128 QYHAYGALALMRQDPPRNEELDAFLSRAVYKITTIOEGPNLMGEAETCARKLLESGLS 187
Oy 254 RANELVNPVVDVDAATATRG-----RSAASRPTERRAPARS 292
Db 188 QGNEVKKSKSERTTKSERTTRRGGEIEIKSPDPGSHHTHNPRTATS 233

RESULT 6
Oy 089247 PRELIMINARY; PRT; 241 AA.
AC 089247:
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE TEGUMENT PROTEIN (UL49 PROTEIN).
GN UL49 OR ORF 57.
OS Galid herpesvirus 1 (serotype 2), and
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OS Gallid herpesvirus 3.
OC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_TaxID=36353, 35250;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Gallid herpesvirus 1 (serotype 2); STRAIN=HPRS 24;
RX MEDLINE=98378051; PubMed=9714249;
RA Izumiya Y., Jang H.-K., Kashiwase H., Cai J.-S., Nishimura Y.,
RA Tsushima Y., Kato K., Miyazawa T., Kai C., Mikami T.;
RT "Identification and transcriptional analysis of the homologues of the
RT herpes simplex virus type 1 UL41 to UL51 genes in the genome of
RT noncogenic Marek's disease virus serotype 2.";
RN J. Gen. Virol. 79:1997-2001(1998).
RL [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Gallid herpesvirus 1 (serotype 2); STRAIN=HPRS24;
RA Jang H., Cai J., Izumiya Y., Murakami Y., Mochizuki M., Song C.,
RA Lee Y., Kai C., Takahashi E., Mikami T.;
RT "The complete DNA sequence and transcription map of the unique long
RT genome region of Marek's disease virus type 2.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Gallid herpesvirus 3; STRAIN=HPRS24;
RA Izumiya Y., Jang H., Ono M., Mikami T.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=Gallid herpesvirus 3; STRAIN=HPRS24;
RA Izumiya Y., Jang H., Ono M., Mikami T.;
RT "A Complete Genomic DNA Sequence of Marek's Disease Virus Type 2,
RT Strain HPRS24.";
RL Curr. Top. Microbiol. Immunol. 0:0-0(2000).
DR EMBL: AB012572; BAA32585.1; -
DR EMBL: AB024414; BAA82945.1; -
DR EMBL: AB049735; BAB16559.1; -
SQ SEQUENCE 241 AA; 26884 MW; 222A0463AAEDF754 CRC64;

Query Match 13.3%; Score 207; DB 12; Length 241;
Best Local Similarity 24.2%; Pred. NO. 4.5e-07;
Matches 68; Conservative 42; Mismatches 95; Indels 76; Gaps 9;

QY 38 DTSRGALQTRSGEVRFYQYDESDYALYGSSSEDEDEPEVPTRRPVGAVLSGPG 97
DB 3 DSDBRKSSRRRSTMR-----TSPNSNAHISTRARRRSS-----KNES 40
QY 98 PARAPPPAGSGAGRTPTTAPRAPRTQRYATKAPAAPAAETTRGRKSAOPESALPDAP 157
DB 41 PDRISP-----PSHSLQRRRSVKIERK---DSSESTORGE-----72
QY 158 ASTAPRTSKTPAAGLAR-KLHFSTAPPNPDAMPPTPRVAGNKNKVFCAAVGLAMHARMA 216
DB 73 SLSSKVAKAGARIEGKRAFTSTTPASATSTRNSNTLVYNERLFCGAAVAAYOYHAYRG 132
QY 217 AVALDMSRPRPTDNLNELLGITTRVYCEGKNLQORANL-----VNPDV-----263
DB 133 ALSLMRNAPRTNAELPEELARAIKITIOEGANLLDEACRECKLSEESGLSPDMGNPK 192
QY 264 -----VQDVDAATATRGSAASRPTERRPAPARSASRR 298
DB 193 SRSGYCKRDGDESTPYDKRD-----RRSKTPGRAPPTTSRR 227

RESULT 7
ID Q9DHC2 PRELIMINARY: PRT; 283 AA.
AC Q9DHC2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE UL49 TEGUMENT PHOSPHOPROTEIN (UL49 TEGUMENT PROTEIN VP22).

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GN HVT057 OR UL49.
OS Meleagrid herpesvirus 1 (herpesvirus of turkeys).
OC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammapherpesvirinae.
OX NCBI_TaxID=37108;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FC126;
RA Alfonso C.L., Tulman E.R., Lu Z., Zsak L., Rock D.L., Kutish G.K.;
RT "The genome of turkey herpesvirus.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FC126;
RA Kingham B.J., Zelnik V., Kopacek J., Majerclak V., Ney E., Chen Y.,
RA Schmidt C.J.;
RT "Coding potential of herpesvirus of turkey: comparative genetic
RT analysis of Marek's disease serologically related viruses.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF291866; AAG45787.1; -
DR EMBL: AF282130; AAG30089.1; -
SQ SEQUENCE 283 AA; 31437 MW; 04A1732AD6746E0 CRC64;

Query Match 12.7%; Score 198; DB 12; Length 283;
Best Local Similarity 29.7%; Pred. NO. 2.2e-06;
Matches 69; Conservative 31; Mismatches 114; Indels 18; Gaps 7;

QY 84 TRRPVSGAVLSGPGPARPPAGSGAGRTPTTA--PRAPRORVATKAPAPAAET--139
DB 31 TRKRSTSLSPDDLYHASRVTSNRHARSPPAELPRSTRQOS-AHHSESPPEERPG 89
QY 140 TRKRKSAOPESALPDAPASTAPRTSKTPAAGLAR-----KLHFSTAPPNPDAMPPT 190
DB 90 PSDBRLQRRKSKVEVEPATSKS-SSIRPLGQARQEVRAVGKNKFEFSSAPTSRSHMK 148
QY 191 PRVAGNKNKVFCAAVGLAMHARMAVOLDMRSRPTDNLNELLGITTRVYCEGKN 250
DB 149 SNTVAFQNHVCCAAVAVARYHAFRGALALMKNKEPPTDQLDFLVRVAVKYTVREGPY 208
QY 251 LLORANLVDVQDVDAATATRGSAASRPTERRPAPARSA--SNRRPV 300
DB 209 LLEBA-ESTQRMETGLGSADNKKPKRSRSGRDEVEGSEGSNSGARRPT 259

RESULT 8
ID Q9NVA2 PRELIMINARY: PRT; 388 AA.
AC Q9NVA2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE XALPHAS PROTEIN (DJ986W20.3.1) (ISOFORM 1 OF GRANINE NUCLEOTIDE
DE BINDING PROTEIN (G PROTEIN), ALPHA STIMULATING ACTIVITY POLYPEPTIDE 1)
DE (FRAGMENT).
GN XALPHAS OR GNAS1.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20215313; PubMed=10749922;
RA Hayward B.E., Bonthron D.T.;
RT "An imprinted antisense transcript at the human GNAS1 locus.";
RL Hum. Mol. Genet. 9:835-841(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ251760; CAB83215.1; -
DR EMBL: AL132655; CAC07997.1; -
DE InterPro: IPR001019; Gprotein_alpha.

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RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HG52;
 RX MEDLINE=92113549; PubMed=1662697;
 RA McGeoch D.J., Cunningham C., McIntyre G., Dolan A.;
 RT "Comparative sequence analysis of the long repeat regions and
 RT adjoining parts of the long unique regions in the genomes of herpes
 RT simplex viruses types 1 and 2."
 RL J. Gen. Virol. 72:3057-3075(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HG52;
 RX MEDLINE=92356101; PubMed=1322965;
 RA Barrett B.C., Dolan A., Telford E.A.R., Davidson A.J., McGeoch D.J.;
 RT "A novel herpes simplex virus gene (UL49) encodes a putative membrane
 RT protein with counterparts in other herpesviruses."
 RL J. Gen. Virol. 73:2167-2171(1992).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HG52;
 RA Dolan A.;
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: Z86099; CAB06722.1; -
 DR InterPro: IPR001109; HupF_HypC.
 SQ SEQUENCE 3122 AA; 330045 MW; 6EBF94B51BE8C0B CRC64;

Query Match 9.6%; Score 149.5; DB 12; Length 3122;
 Best Local Similarity 26.1%; Pred. No. 0.069;
 Matches 74; Conservative 22; Mismatches 110; Indels 77; Gaps 11;

QY 75 DDEHEVPTRRRPVSGAVLSGCPARAPPPPGSGGAGRTPTTAPAPPTORVATK----- 130
 DB 2633 DDPREPPTRPPSPADAL-----PPPAFSGSAAAFSAVPVRSKRTRAKSRAP 2682
 QY 131 -----APAAPAETTR-GKRSAPESA-----ALPDAPAST-----A 161
 DB 2683 RASAPPEGRRPALPAPVAPVAAASARPPDPPTESAPAMWSALPLPGPASARGAFPA 2742
 QY 162 PTRS---KTPAGCLA-----RKLHFTAPRPDAPWTPRVAAGFKRVCAGVGLAAM 211
 DB 2743 PTLAPIPPPAEGAVVPGGDRRRGRQTAGSPPPRGP-AAAGPRRLTRPAVASLSA- 2800
 QY 212 HARMAVOLMDMSRPTDEDNLGLITITRVTCGEG---KNLQRLANELVNP----- 262
 DB 2801 -----SINSLPSPRPDPADHAAVSAALAAVPPSPGLAPPTSAVOTSPPLAPGVPAS 2853
 QY 263 -----VQDVDAATATGRSAASRPTERRAPARSASRRRP 299
 DB 2854 EPLCGWVPGPVARRPPSPATKPAARTRIRARSVPPPLP 2896

RESULT 14
 O56868 PRELIMINARY; PRT; 266 AA.
 ID O56868;
 AC O56868;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PUTATIVE VIRAL TEGUMENT PROTEIN.
 GN UL49.
 OS gallid herpesvirus 1.
 OC Viruses: dsDNA viruses, no RNA stage: Herpesviridae;
 OC Alphaherpesvirinae; Varicelloviruses.
 OX NCBI_TaxId=10386;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98080487; PubMed=9420298;
 RA Ziemann K., Mettenleiter T.C., Fuchs W.;
 RT "Gene arrangement within the unique long genome region of infectious
 RT latyngotracheitis virus is distinct from that of other
 RT alphaherpesviruses."
 RL J. Virol. 72:847-852(1998).

DR EMBL: Y14300; CAA74678.1; -
 DR InterPro: IPR001917; AminoTransf_2.
 DR PROSITE: PS00599; AA_TRANSFER_CLASS_2; UNKNOWN.1.
 SQ SEQUENCE 266 AA; 30358 MW; FF0459DAE1C6F4A9 CRC64;

Query Match 9.5%; Score 148; DB 12; Length 266;
 Best Local Similarity 21.6%; Pred. No. 0.0058;
 Matches 59; Conservative 33; Mismatches 113; Indels 68; Gaps 8;

QY 68 YGGSSEDEHPEVPRTRPPVSGAVLSGCPARAPP----- 105
 DB 4 YDLSEAKKYHDDTTRRRDDT-----TRRPKPQFHEPWSGSRRTSPYLDLRGSD 54
 QY 106 --AGSGAGRTPTTARARTQVATKAPAAETTRKRSQAPESALPDAPASTPT 163
 DB 55 SDSSEGDYH-----PSRAHYSRDHTAPP-----QGRSRPMSFKETTPKEEPPQ 101
 QY 164 RSK-----TPAQLARKLHF-----STAPPNDAPWTPRVAGFNKRVCAVGLAAMH 212
 DB 102 SKRGWNPDMHCAGIMRRLITSGFGSATPSCGDEDPWHTSTIPANRSATVQAVSTAMQ 161
 QY 213 ARMAVOLMDMSRPTDEDNLGLITITRVTCGCKNLLQRLANELVNPVQVDDAATA 272
 DB 162 AELIAREVMDVTKPTNRELMDVRELITIIINPESIMS-----VATSVARAIKEGP 216
 QY 273 TGRSAASRPTERR-----APARSASRRRP 299
 DB 217 ITHELLOKRRSKPPTRRKTEGDGARRSSSRSPQ 249

RESULT 15
 Q9RVT4 PRELIMINARY; PRT; 395 AA.
 ID Q9RVT4;
 AC Q9RVT4;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE HYPOHETICAL 40.0 KDA PROTEIN.
 GN DR0938.
 OC Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
 OX NCBI_TaxId=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-R1;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Uitterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans R1."
 RL Science 286:1571-1577(1999).
 DR EMBL: AE001946; AAF10516.1; -
 DR TIGR: DR0938; -
 DR InterPro: IPR002965; P-rich_extensn.
 DR PRINTS: PR01217; PRICHEXTENSN.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 395 AA; 40003 MW; 75FD9637171DAAFP0 CRC64;

Query Match 9.4%; Score 146.5; DB 16; Length 395;
 Best Local Similarity 25.1%; Pred. No. 0.011;
 Matches 80; Conservative 23; Mismatches 133; Indels 83; Gaps 13;
 QY 6 SVKSGPREVPDEYEDLYTPSSGMASSPSPDTSRRGLQTRSRORGEVRYVQIDESDY 65
 DB 44 SLILGERRAPAPVPG-----APQPTTSIPVSPGAVVADGSPQTAAPAOAQT----- 90

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OY 66 ALYGSSSEDDHEVPRTRRPVSGAVLSGPGAPAPPPPPAGSGAGRTT-----TTAP 119
Db 91 ---AGKIPPAAPAPAKIPPVL-----PERRMPAPP-----TPRPVEETTTA 133
OY 120 RAPRTORVATKAPA-----APAEETTRGKSAOPESALPDAPASTATRSKTPAQGL 172
Db 134 ASPTTQPPVTQAPATOTPTPTQTPAQAQAPATQPPATP--APEPAAPAEAPATTPPEPAT-- 189
OY 173 ARKLHSTAPPNPDAPWTPRVA-----GFNKRVECAVGRILAAHARMAAVQIWDMS 224
Db 190 -----PTEPAAP-APGTPAVAPSAQRTPLRSDYRVMLGTFGSEALRSATAGV----- 236
OY 225 RPRDDELNELGITTIRVTVCCKNLOR---ANELVNPVYQVYDAATATGRSAS 280
Db 237 -----SALGYTVYVIDL--GNOFVAVQVGPFADEASGQAADIRRAYARARELYPPR 285
OY 281 RPTERRAPAPASASRP RP 299
Db 286 GQTLRNPAAPAAAAPATP 304
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Search completed: August 28, 2002, 12:27:39
Job time: 238 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 12:27:42 ; Search time 108.25 Seconds

(without alignments)
978.717 Million cell updates/sec

Title: US-09-522-278b-12

Perfect score: 1561

Sequence: 1 MTSRRSYKSGPREVDEYE.....PTERRPARASAPRRVE 301

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 2352106

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/2/paa/US06.COMB.pep: *
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26: /cgn2_6/ptodata/2/paa/US60.COMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	179	11.5	37	13	US-08-902-572-16
2	179	11.5	37	14	US-09-063-657-18
3	179	11.5	37	17	US-09-320-912B-49
4	179	11.5	37	17	US-09-347-504-14
5	179	11.5	37	18	US-09-415-795-27
6	179	11.5	37	21	US-09-718-233-16
7	169	10.8	34	14	US-09-011-073-2

8	169	10.8	34	16	US-09-229-486-2	Sequence 2, Appl1
9	169	10.8	34	21	US-09-773-430-2	Sequence 2, Appl1
10	169	10.8	34	24	US-10-083-889-19	Sequence 19, Appl1
11	166	10.6	34	21	US-09-780-070-39	Sequence 39, Appl1
12	73	4.7	48	20	US-09-617-682A-15494	Sequence 13494, A
13	69.5	4.5	48	24	US-10-029-386-31973	Sequence 31973, A
14	68.5	4.4	48	22	US-09-880-578-32	Sequence 32, Appl1
15	67.5	4.3	47	21	US-09-708-477-6419	Sequence 46419, A
16	65	4.2	49	22	US-09-855-754-14	Sequence 14, Appl1
17	64.5	4.1	42	7	US-08-322-768A-23	Sequence 23, Appl1
18	64.5	4.1	48	22	US-09-855-754-20	Sequence 20, Appl1
19	64	4.1	48	1	PCR-US01-08631-35222	Sequence 35222, A
20	64	4.1	48	20	US-09-688-051-1876	Sequence 1876, Ap
21	64	4.1	50	1	PCR-US99-17738-21	Sequence 21, Appl1
22	63	4.0	49	1	PCR-US97-14834-11	Sequence 11, Appl1
23	63	4.0	49	13	US-08-916-246-11	Sequence 11, Appl1
24	63	4.0	49	23	US-09-949-186-11	Sequence 11, Appl1
25	62.5	4.0	43	20	US-09-617-681A-1322	Sequence 1322, Ap
26	62	4.0	35	14	US-09-050-861A-13	Sequence 13, Appl1
27	62	4.0	45	15	US-09-192-433-56	Sequence 56, Appl1
28	62	4.0	50	21	US-09-766-692-2303	Sequence 2303, Ap
29	61	3.9	50	26	US-60-213-162-126	Sequence 126, App
30	60.5	3.9	46	19	US-09-583-110-4648	Sequence 4648, Ap
31	60.5	3.9	48	1	PCR-US00-06830-133	Sequence 133, App
32	60.5	3.9	49	16	US-09-270-767-16437	Sequence 36437, A
33	60.5	3.9	49	16	US-09-270-767-51654	Sequence 51654, A
34	60.5	3.9	49	16	US-09-270-849B-185006	Sequence 185006, A
35	60	3.8	45	13	US-08-961-520-53	Sequence 53, Appl1
36	60	3.8	45	21	US-09-708-427-45178	Sequence 45178, A
37	59	3.8	35	17	US-09-396-347B-11	Sequence 11, Appl1
38	59	3.8	35	17	US-09-396-347B-42	Sequence 42, Appl1
39	59	3.8	35	17	US-09-396-347D-11	Sequence 11, Appl1
40	59	3.8	35	17	US-09-396-347D-42	Sequence 42, Appl1
41	59	3.8	39	6	US-08-247-544-2	Sequence 2, Appl1
42	58.5	3.7	50	21	US-09-708-427-57629	Sequence 57629, A
43	58.5	3.7	40	24	US-10-029-386-33404	Sequence 33404, A
44	58.5	3.7	42	22	US-09-855-754-23	Sequence 23, Appl1
45	58.5	3.7	48	20	US-09-688-051-2166	Sequence 2166, Ap

ALIGNMENTS

RESULT 1
US-08-902-572-16
; Sequence 16, Application US/08902572
; GENERAL INFORMATION:
; APPLICANT: Gyuris, Jeno
; APPLICANT: Lamphere, Lou
; APPLICANT: Beach, David H.
; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HONG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,572
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-069, 03

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-902-572-16

Query Match
Best Local Similarity 100.0%; Score 179; DB 13; Length 37;
Pred. No. 2.7e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 DVDATATRGSAASRPTERRAPARSASRRPRVE 301
DB 2 DVDATATRGSAASRPTERRAPARSASRRPRVE 37

RESULT 2
US-09-063-657-18
; Sequence 18, Application US/09063657
; GENERAL INFORMATION:
; APPLICANT: Hannon, Gregory J.
; APPLICANT: Wang, Jing
; APPLICANT: Beach, David H.
; TITLE OF INVENTION: EXTENSION OF CELLULAR LIFESPAN, METHODS AND REAGENTS
; FILE REFERENCE: CSV-008.01
; CURRENT APPLICATION NUMBER: US/09/063,657
; CURRENT FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 37
; TYPE: PRT
; ORGANISM: HSV-1
; FEATURE:
; OTHER INFORMATION: VP22
; US-09-063-657-18

Query Match
Best Local Similarity 100.0%; Score 179; DB 14; Length 37;
Pred. No. 2.7e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 DVDATATRGSAASRPTERRAPARSASRRPRVE 301
DB 2 DVDATATRGSAASRPTERRAPARSASRRPRVE 37

RESULT 3
US-09-320-912B-49
; Sequence 49, Application US/09320912B
; GENERAL INFORMATION:
; APPLICANT: Hannon, G.
; APPLICANT: Wang, J.
; APPLICANT: Beach, D.
; TITLE OF INVENTION: EXTENSION OF CELLULAR LIFESPAN, METHODS AND REAGENTS
; FILE REFERENCE: CSHL-P02-008
; CURRENT APPLICATION NUMBER: US/09/320,912B
; CURRENT FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 09/063,657
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; US-09-320-912B-49

Query Match
Best Local Similarity 100.0%; Score 179; DB 17; Length 37;
Pred. No. 2.7e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 DVDATATRGSAASRPTERRAPARSASRRPRVE 301
DB 2 DVDATATRGSAASRPTERRAPARSASRRPRVE 37

RESULT 4
US-09-347-504-14
; Sequence 14, Application US/09347504
; GENERAL INFORMATION:
; APPLICANT: Howley, Peter M.
; APPLICANT: Benson, John
; APPLICANT: Kasukawa, Hiroaki
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE REFERENCE: HMV-041.01
; CURRENT APPLICATION NUMBER: US/09/347,504
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VP22
; US-09-347-504-14

Query Match
Best Local Similarity 100.0%; Score 179; DB 17; Length 37;
Pred. No. 2.7e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 DVDATATRGSAASRPTERRAPARSASRRPRVE 301
DB 2 DVDATATRGSAASRPTERRAPARSASRRPRVE 37

RESULT 5
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; Sequence 27, Application US/09415795
; GENERAL INFORMATION:
; APPLICANT: Zhou, Pengbo
; APPLICANT: Howley, Peter M.
; TITLE OF INVENTION: TARGETED PROTEOLYSIS BY RECRUITMENT TO UBIQUITIN
; FILE REFERENCE: HMV-043.01
; CURRENT APPLICATION NUMBER: US/09/415,795
; CURRENT FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VP22 (C-terminal domain)
; US-09-415-795-27

Query Match
Best Local Similarity 100.0%; Score 179; DB 18; Length 37;
Pred. No. 2.7e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db       2 DVDATATRGSRASRPTERRAPARPSASRRPRPVE 37
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1      RESULT 6
2      US-09-718-233-16
3      : Sequence 16, Application US/09/18233
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5      : GENERAL INFORMATION:
6      :
7      : APPLICANT: Gyuris, Jeno
8      :               Lamphere, Lou
9      :               Beach, David H.
10     :
11     : TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
12     : RELATED THEREOF
13     :
14     : NUMBER OF SEQUENCES: 34
15     :
16     : CORRESPONDENCE ADDRESS: 34
17     :
18     : ADDRESSEE: FOLEY, HOAG & ELIOT LLP
19     :
20     : STREET: One Post Office Square
21     :
22     : CITY: Boston
23     :
24     : STATE: MA
25     :
26     : COUNTRY: USA
27     :
28     : ZIP: 02109-2170
29     :
30     : COMPUTER READABLE FORM:
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36     : OPERATING SYSTEM: PC-DOS/MS-DOS
37     :
38     : SOFTWARE: PatentIn Release #1.0, Version #1.30
39     :
40     : CURRENT APPLICATION DATA:
41     :
42     : APPLICATION NUMBER: US/09/718,233
43     :
44     : FILING DATE: 21-Nov-2000
45     :
46     : CLASSIFICATION: <Unknown>
47     :
48     : ATTORNEY/AGENT INFORMATION:
49     :
50     : NAME: Vincent, Matthew P.
51     :
52     : REGISTRATION NUMBER: 36,709
53     :
54     : REFERENCE/DOCKET NUMBER: MIV-069.03
55     :
56     : TELECOMMUNICATION INFORMATION:
57     :
58     : TELEPHONE: 617-832-1000
59     :
60     : TELEFAX: 617-832-7000
61     :
62     : INFORMATION FOR SEQ ID NO: 16:
63     :
64     : SEQUENCE CHARACTERISTICS:
65     :
66     : LENGTH: 37 amino acids
67     :
68     : TYPE: amino acid
69     :
70     : STRANDEDNESS: <Unknown>
71     :
72     : TOPOLOGY: linear
73     :
74     : MOLECULE TYPE: peptide
75     :
76     : SEQUENCE DESCRIPTION: SEQ ID NO: 16:
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Query Match	11.5%	Score 179	DB 21	length 37
Best Local Similarity	100.0%	Pred. No. 2,7e-05		
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0				
QY	266	DYDAATATGCRSAASRPTEPRAPARSAASRP RPVE	301	
	2	DYDAATATGCRSAASRPTEPRAPARSAASRP RPVE	37	

```

1  RESULT 7
2  US-09-011-073-2
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4  ; Sequence 2, Application US/09011073
5  ; GENERAL INFORMATION:
6  ; APPLICANT: O'Hare et al.
7  ; TITLE OF INVENTION: TRANSPORT PROTEINS AND THEIR USES
8  ; NUMBER OF SEQUENCES: 2
9  ; CORRESPONDENCE ADDRESS:
10 ; ADDRESSEE: Klariquist Sparkman Campbell Leigh &
11 ; ADDRESSEE: Winston, LLP
12 ; STREET: One World Trade Center
13 ; STREET: 121 S.W. Salmon Street
14 ; STREET: Suite 1600
15 ; CITY: Portland
16 ; STATE: Oregon

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1  COUNTRY: United States of America
2  ZIP: 97204-2988
3
4  COMPUTER READABLE FORM:
5  MEDIUM TYPE: Disk, 3-1/2 inch
6  COMPUTER: IBM PC compatible
7  OPERATING SYSTEM: MS DOS
8  SOFTWARE: WordPerfect 7.0 & ASCII
9
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/09/011.073
12 FILING DATE:
13
14 CLASSIFICATION: 424
15
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: PCT/GB96/01831
18 FILING DATE: JULY 25, 1996
19
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Earp, David J.
22 REGISTRATION NUMBER: 41,401
23 REFERENCE/DOCKET NUMBER: 5759-49294/DJE
24
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (503) 226-7391
27 TELEFAX: (503) 228-9446
28
29 INFORMATION FOR SEQ ID NO. 2:
30 SEQUENCE CHARACTERISTICS:
31     LENGTH: 34
32     TYPE: amino acid
33     STRANDEDNESS: single
34     TOPOLOGY: linear
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Query Match	10.8%;	Score 169;	DB 14;	Length 34;
Best Local Similarity	100.0%;	Pred. No. 0.00012;		
Matches 34;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Oy      268 DATATGRSASRPTERRPARPARSASRRPRPVE 30I  
        |||||  
Db       1 DATATRGRSASRPTERRPARPARSASRRPRPVE 34
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RESULT 8
 US-09-229-486-2
 Sequence 2, Application US/09229486
 GENERAL INFORMATION:
 APPLICANT: O'Hare et al.
 TITLE OF INVENTION: Transport proteins and their uses
 FILE REFERENCE: 51446
 CURRENT APPLICATION NUMBER: US/09/229,486
 CURRENT FILING DATE: 1999-01-13
 EARLIER APPLICATION NUMBER: PCT/GB96/01831
 EARLIER FILING DATE: 1996-07-25
 EARLIER APPLICATION NUMBER: GB 9601570.6
 EARLIER FILING DATE: 1996-01-26
 EARLIER APPLICATION NUMBER: GB 9515568.5
 EARLIER FILING DATE: 1995-07-28
 EARLIER APPLICATION NUMBER: US 09/011,073
 EARLIER FILING DATE: 1998-01-26
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 34
 TYPE: PRT
 ORGANISM: herpes simplex virus type 1
 US-09-229-486-2

Query Match	10.8%	Score 169	DB 16	Length 34
Best Local Similarity	100.0%	Pred. No. 0.00012		
Matches 34	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	268	DAATATGCRASAPTERPRAPASASAPRRPVE	301	
db	1	DAATATGCRASAPTERPRAPASASAPRRPVE	34	

RESULT 9
US-09-773-430-2
; Sequence 2, Application US/09773430
; GENERAL INFORMATION:
; APPLICANT: O'Hare et al.
; TITLE OF INVENTION: TRANSPORT PROTEINS AND THEIR USES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; Whinston, LLP
; STREET: One World Trade Center
; 121 S.W. Salmon Street
; Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204-2988
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 7.0 & ASCII
; CURRENT APPLICATION DATA: US/09/773,430
; APPLICATION NUMBER: US/09/773,430
; FILING DATE: 31-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/011,073
; FILING DATE: 1998-07-26
; ATTORNEY/AGENT INFORMATION:
; NAME: Earp, David J.
; REGISTRATION NUMBER: 41,401
; REFERENCE/DOCKET NUMBER: 5759-49294/DUE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-773-430-2

Query Match 10.8%; Score 169; DB 21; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 268 DAATATGRSASRPTERRPAPARSRRRPVE 301
|||||
Db 1 DAATATGRSASRPTERRPAPARSRRRPVE 34

RESULT 10
US-10-083-889-19
; Sequence 19, Application US/10083889
; GENERAL INFORMATION:
; APPLICANT: Zahner, Joseph E.
; TITLE OF INVENTION: Inhibitor of cell proliferation and methods of use thereof.
; FILE REFERENCE: 16850-7331
; CURRENT APPLICATION NUMBER: US/10/083,889
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/271,798
; PRIOR FILING DATE: 2001-02-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 19
; LENGTH: 34
; TYPE: PRT
; ORGANISM: mammal

US-10-083-889-19

Query Match 10.8%; Score 169; DB 24; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 268 DAATATGRSASRPTERRPAPARSRRRPVE 301
|||||
Db 1 DAATATGRSASRPTERRPAPARSRRRPVE 34

RESULT 11
US-09-780-070-39
; Sequence 39, Application US/09780070
; GENERAL INFORMATION:
; APPLICANT: Burke, James
; APPLICANT: Stiltwater, Warren
; APPLICANT: Nagai, Yoshitaka
; TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPE
; FILE REFERENCE: 5405.242
; CURRENT APPLICATION NUMBER: US/09/780,070
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/189,781
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 34
; TYPE: PRT
; ORGANISM: herpes simplex virus type 1
US-09-780-070-39

Query Match 10.6%; Score 166; DB 21; Length 34;
Best Local Similarity 97.1%; Pred. No. 0.00019;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 268 DAATATGRSASRPTERRPAPARSRRRPVE 301
|||||
Db 1 DAATATGRSASRPTERRPAPARSRRRPVD 34

RESULT 12
US-09-617-682A-15494
; Sequence 15494, Application US/09617682A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
; FILE REFERENCE: 2750-1063P
; CURRENT APPLICATION NUMBER: US/09/617,682A
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 16871
; SEQ ID NO 15494
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..48
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..48
; OTHER INFORMATION: Ceres Seq. ID 1424260
US-09-617-682A-15494

Query Match 4.7%; Score 73; DB 20; Length 48;
Best Local Similarity 45.0%; Pred. No. 8.6e+02;
Matches 18; Conservative 5; Mismatches 15; Indels 2; Gaps 2;

OY 96 PGPAPPPGSGGAGRTPTTAPRAPRTQVATKAPAP 135
 DB 11 PGSA-SPSSPGSTGSARPTTASTAP-PATTTTNSPADP 48

RESULT 13 US-10-029-386-31973

; Sequence 31973, Application US/10029386
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Hank, David R.
 ; APPLICANT: Hanzel, David K.
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
 ; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
 ; FILE REFERENCE: AECOMICA-X-2
 ; CURRENT APPLICATION NUMBER: US/10/029,386
 ; CURRENT FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 34288
 ; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 31973
 ; LENGTH: 43
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO AL137784.2
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
 ; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.92
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
 ; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7

US-10-029-386-31973

Query Match 4.5%; Score 69.5; DB 24; Length 43;
 Best Local Similarity 50.0%; Pred. No. 1.3e+03;
 Matches 15; Conservative 4; Mismatches 8; Indels 3; Gaps 1;

OY 272 ATRGSSASRPTERRAPAR---SASRP 298
 DB 4 AVRGRASSARPLRP RP RP RP RP RP RP RP 33

RESULT 14 US-09-880-578-32

; Sequence 32, Application US/09880578
 ; GENERAL INFORMATION:
 ; APPLICANT: Lok, Si
 ; APPLICANT: Presnell, Scott R.
 ; APPLICANT: Jelmeberg, Anna C.
 ; APPLICANT: Gilbert, Teresa
 ; APPLICANT: Foster, Donald C.
 ; APPLICANT: Adams, Robyn L.
 ; APPLICANT: Lehnert, Joyce M.

; TITLE OF INVENTION: MAMMALIAN ZCYTORS
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Zymogenetics
 ; STREET: 1201 Eastlake Ave East
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98102

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: PASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/880,578
 FILING DATE: 13-Jun-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G

REGISTRATION NUMBER: 32,743

REFERENCE/DOCKET NUMBER: 96-22

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627

TELEFAX: 206-442-6678

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 48 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-09-880-578-32

Query Match 4.4%; Score 68.5; DB 22; Length 48;
 Best Local Similarity 37.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 5; Mismatches 14; Indels 15; Gaps 3;

OY 98 PARAPPPGSGGAGRTPTTAPRAPRTQVATKAPAPAEETTRGKSAOPESA 151
 DB 9 PPRAPPPS-----RSP---PRAPGS-----AGPMPAGMPAGRCGPAAQSA 47

RESULT 15 US-09-708-427-46419

; Sequence 46419, Application US/09708427
 ; GENERAL INFORMATION:
 ; APPLICANT: N. ALEXANDROV et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
 ; TITLE OF INVENTION: THEREBY
 ; FILE REFERENCE: 2750-1243P
 ; CURRENT APPLICATION NUMBER: US/09/708,427
 ; CURRENT FILING DATE: 2000-11-09
 ; NUMBER OF SEQ ID NOS: 85364
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 46419
 ; LENGTH: 47
 ; TYPE: PRT
 ; ORGANISM: Zea mays subsp. mays
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: 1..47
 ; OTHER INFORMATION: Xaa is any amino acid
 ; NAME/KEY: misc.feature
 ; LOCATION: 1..47
 ; OTHER INFORMATION: Ceres Seq. ID 1852321
 ; US-09-708-427-46419

US-09-708-427-46419

Query Match 4.3%; Score 67.5; DB 21; Length 47;
 Best Local Similarity 39.5%; Pred. No. 2e+03;
 Matches 17; Conservative 4; Mismatches 15; Indels 7; Gaps 2;

OY 79 PEVPRTRRPVSGAVLSGPP-ARAPPPGSGGAGTPTTAR 120
 DB 10 PPLPSKRPAPAGIPTSPGSR LAPL-----KKPTLAPR 46

Search completed: August 28, 2002, 12:31:12
 Job time: 210 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 12:26:21 ; Search time 13.08 Seconds
(without alignments)
562.087 Million cell updates/sec

Title: US-09-522-278B-12

Perfect score: 1561
Sequence: 1 MTSRRSVKSGPREVPDEYE.....PTERRAPARSAPRRPVE 301

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 164183

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PC10S.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	169	10.8	34	US-09-011-073A-2	Sequence 2, Appl1
2	166	10.6	32	US-09-230-421-14	Sequence 14, Appl1
3	117	7.5	20	US-09-230-421-6	Sequence 6, Appl1
4	108	6.9	20	US-09-230-421-5	Sequence 5, Appl1
5	106	6.8	20	US-09-230-421-9	Sequence 9, Appl1
6	103	6.6	20	US-09-230-421-7	Sequence 7, Appl1
7	103	6.6	20	US-09-230-421-8	Sequence 8, Appl1
8	100	6.4	20	US-09-230-421-11	Sequence 11, Appl1
9	99	6.3	20	US-09-230-421-10	Sequence 10, Appl1
10	89	5.7	20	US-09-230-421-12	Sequence 12, Appl1
11	73	4.7	48	US-09-071-224-32	Sequence 4, Appl1
12	68.5	4.4	48	US-09-071-224-32	Sequence 32, Appl1
13	65.5	4.2	48	5171685-7	Patent No. 5171685
14	65.5	4.2	48	5518916-7	Patent No. 5518916
15	64.5	4.1	42	US-08-476-866-23	Sequence 23, Appl1
16	62	4.0	45	US-08-676-279-56	Sequence 56, Appl1
17	59	3.8	35	US-09-001-984C-11	Sequence 11, Appl1
18	59	3.8	35	US-09-001-984C-42	Sequence 42, Appl1
19	58	3.7	48	US-07-609-716-106	Sequence 106, App
20	58	3.7	48	US-08-475-411A-106	Sequence 106, App
21	58	3.7	48	US-08-478-029A-106	Sequence 106, App
22	55.5	3.6	33	US-09-071-224-33	Sequence 33, Appl1
23	55	3.5	33	US-08-237-716-11	Sequence 11, Appl1
24	54.5	3.5	46	US-08-483-533-30	Sequence 30, Appl1
25	54.5	3.5	46	US-09-283-471A-30	Sequence 30, Appl1
26	53	3.4	48	US-09-314-268-164	Sequence 164, App
27	52	3.3	20	US-09-010-928B-9	Sequence 9, Appl1

28	52	3.3	34	1	US-08-433-854-12	Sequence 12, Appl1
29	52	3.3	34	1	US-08-174-745A-12	Sequence 12, Appl1
30	52	3.3	34	2	US-08-195-947-12	Sequence 12, Appl1
31	52	3.3	34	2	US-08-433-885-12	Sequence 12, Appl1
32	52	3.3	34	2	US-08-433-908B-12	Sequence 12, Appl1
33	52	3.3	34	4	US-08-410-614-12	Sequence 12, Appl1
34	51.5	3.3	40	4	US-09-314-268-165	Sequence 165, App
35	51.5	3.3	41	1	US-07-609-716-57	Sequence 57, Appl1
36	51.5	3.3	41	1	US-08-642-255-27	Sequence 27, Appl1
37	51.5	3.3	41	4	US-08-475-411A-57	Sequence 57, Appl1
38	51.5	3.3	41	4	US-08-478-029A-57	Sequence 57, Appl1
39	51	3.3	24	1	US-08-031-148-5	Sequence 5, Appl1
40	51	3.3	24	2	US-08-306-078-2	Sequence 2, Appl1
41	51	3.3	24	3	US-08-415-838-5	Sequence 5, Appl1
42	51	3.3	40	4	US-08-672-213-29	Sequence 29, Appl1
43	50.5	3.2	36	1	US-07-972-032-67	Sequence 67, Appl1
44	50.5	3.2	36	1	US-08-642-255-79	Sequence 79, Appl1
45	50.5	3.2	40	1	US-08-099-354-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-011-073A-2
Sequence 2 Application US/09011073A
Patent No. 6184038
GENERAL INFORMATION:
APPLICANT: O-Chate et al.
TITLE OF INVENTION: TRANSPORT PROTEINS AND THEIR USES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh &
ADDRESS: Winston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
CITY: Suite 1600
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204-2988
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 7.0 & ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011.073A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01831
FILING DATE: JULY 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Earp, David J.
REGISTRATION NUMBER: 41,401
REFERENCE/DOCKET NUMBER: 5759-49294/DJE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 34
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
US-09-011-073A-2

Query Match 10.8%; Score 169; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 268 DAATATGRGSASRPTERRPARASRRPRPYE 301
      |||||||
DB 1 DAATATGRGSASRPTERRPARASRRPRPYE 34

RESULT 2
US-09-230-421-14
; Sequence 14, Application US/09230421.
; Patent No. 6200577
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
; OTHER INFORMATION: SEQUENCE
US-09-230-421-14

Query Match 10.6%; Score 166; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 190 TPRVAGFNKRVCFAVGRLLAAMHARMAAVQLW 221
      |||||||
DB 1 TPRVAGFNKRVCFAVGRLLAAMHARMAAVQLW 32

RESULT 3
US-09-230-421-6
; Sequence 6, Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
; OTHER INFORMATION: SEQUENCE
US-09-230-421-6

Query Match 7.5%; Score 117; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 178 ESTAPPNPDAWMTPRVAGFN 197
      |||||||
DB 1 ESTAPPNPDAWMTPRVAGFN 20

RESULT 4
US-09-230-421-5
; Sequence 5, Application US/09230421
; Patent No. 6200577
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; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
; OTHER INFORMATION: SEQUENCE
US-09-230-421-5

Query Match 6.9%; Score 108; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 166 KTPAGGLARKLHSTAPPNP 185
      |||||||
DB 1 KTPAGGLARKLHSTAPPNP 20

RESULT 5
US-09-230-421-9
; Sequence 9, Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
; OTHER INFORMATION: SEQUENCE
US-09-230-421-9

Query Match 6.8%; Score 106; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 214 RMAAVQLWMSRPRTDEDLN 233
      |||||||
DB 1 RMAAVQLWMSRPRTDEDLN 20

RESULT 6
US-09-230-421-7
; Sequence 7, Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASTSEQ for Windows Version 3.0
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RESULT 11
US-09-230-421-4
; Sequence 4, Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
US-09-230-421-4

Query Match 4.7%; Score 73; DB 4; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.2;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 158 ASTAPTRSKTPAOGLA 173
| | | | | | | | | | | | | | | | | | | | | |
Db 5 ARTAPTRSKTPAOGLA 20

RESULT 12
US-09-071-224-32
; Sequence 32, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, SI
; APPLICANT: Presnell, Scott R.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Rodyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678

TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-224-32

Query Match 4.4%; Score 68.5; DB 4; Length 48;
Best Local Similarity 37.0%; Pred. No. 16;
Matches 20; Conservative 5; Mismatches 14; Indels 15; Gaps 3;

OY 98 PARAPPPAGSGAGRRPTTAPAPRTQVATKAPAPAEITTRGKSAQESA 151
| | | | | | | | | | | | | | | | | | | | | |
Db 9 PRAPPPPPS-----RSP---PRAPGS-----AGPMAGPMAGRGRAQSA 47

RESULT 13
5171685-7
; Patent No. 5171685
; APPLICANT: MCELMAN, TERRY F.; HINES, STEPHEN A.; MCGUIRE,
; TRAVIS C.; PALMER, GUY H.; JASMER, DOUGLAS P.; REDUKER, DAVID W.
; GOFF, WILL L.; PERRYMAN, LANCE E.; DAVIS, WILLIAM C.
; TITLE OF INVENTION: CLONING OF THE BABESIA BOVIS 60 KD ANTIGEN
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/504,461
; FILING DATE: 04-APR-1990
; SEQ ID NO: 7
; LENGTH: 48
5171685-7

Query Match 4.2%; Score 65.5; DB 6; Length 48;
Best Local Similarity 35.1%; Pred. No. 30;
Matches 20; Conservative 5; Mismatches 21; Indels 11; Gaps 2;

OY 132 PAPAPAEITTRGKSAQESALPDAPASTAPTRSKTPAOGLAARKLHFTAPPPDPAP 188
| | | | | | | | | | | | | | | | | | | | | |
Db 1 PQRP-AETQOTQDSAASTPAPSPQRAET-----QQTQDSTAPGTPAAP 46

RESULT 14
5518916-7
; Patent No. 5518916
; APPLICANT: MCELMAN, TERRY F.; MCGUIRE, TRAVIS C.; JASMER,
; DOUGLAS P.; REDUKER, DAVID W.; GOFF, WILL L.; STILLNER, DAVID
; TITLE OF INVENTION: CLONED BABESIA DNA
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,480
; FILING DATE: 21-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 989,616
; FILING DATE: 14-DEC-1992
; APPLICATION NUMBER: 504,461
; FILING DATE: 04-APR-1990
; APPLICATION NUMBER: 333,155
; FILING DATE: 04-APR-1989
; SEQ ID NO: 7
; LENGTH: 48
5518916-7

Query Match 4.2%; Score 65.5; DB 6; Length 48;
Best Local Similarity 35.1%; Pred. No. 30;
Matches 20; Conservative 5; Mismatches 21; Indels 11; Gaps 2;

OY 132 PAPAPAEITTRGKSAQESALPDAPASTAPTRSKTPAOGLAARKLHFTAPPPDPAP 188
| | | | | | | | | | | | | | | | | | | | | |

Db 1 PORP-AETQOTODSAPSTPAAPSPQRPAPT-----QOTQDSTAPGTPAAP 46

RESULT 15
US-08-476-866-23
; Sequence 23, Application US/08476866
; Patent No. 5994339
; GENERAL INFORMATION:
; APPLICANT: CRAPO, JAMES D.
; APPLICANT: FRIDOVICH, IRWIN
; APPLICANT: OURY, TIM
; APPLICANT: DAY, BRIAN J.
; APPLICANT: FOLZ, RODNEY J.
; APPLICANT: FREEMAN, BRUCE A.
; TITLE OF INVENTION: SUPEROXIDE DISMUTASE AND MIMETICS THEREOF
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P. C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,866
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/322,766
; FILING DATE: 13-OCT-1994
; APPLICATION NUMBER: US 08/136,207
; FILING DATE: 15-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-74
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-476-866-23

Query Match 4.1%; Score 64.5; DB 2; Length 42;
Best Local Similarity 36.6%; Pred. No. 31;
Matches 15; Conservative 7; Mismatches 18; Indels 1; Gaps 1;

Qy 103 PPPAGSGAGRTTAPRAP-RTQRYATKAPAPAAETTRG 142
| : || : : | : | : |||| : | : |
Db 1 PASSSSGSLRPAPSSSTPSPWRASRSPRYAPAPSTCTSSG 41

Search completed: August 28, 2002, 12:28:53
Job time: 152 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 12:24:01 ; Search time 13.42 Seconds

(without alignments)
868.449 Million cell updates/sec

Title: US-09-522-278b-12

Perfect score: 1561

Sequence: 1 MTSRSRVKSGPREVPRDEYE.....PTERRAPARSASRRPRVE 301

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1561	100.0	301	1	UL49_HSV11
2	303	19.4	304	1	UL49_HSVB
3	271.5	17.4	258	1	UL49_HSVBC
4	270.5	17.3	290	1	UL49_HSVB4
5	225.5	14.4	302	1	UL49_VZVD
6	166	10.6	1461	1	IE18_PRVIF
7	161.5	10.3	660	1	YH1_EBV
8	153.5	9.8	1446	1	IE18_PRVKA
9	142.5	9.1	263	1	ICP3_HSV1F
10	138	8.8	806	1	MK07_MOUSE
11	135	8.6	261	1	RUL_HSV2H
12	134.5	8.6	3149	1	TEG0_EBV
13	133.5	8.5	852	1	WS14_HUMAN
14	133	8.6	1509	1	GSRI_HUMAN
15	130.5	8.4	591	1	PAK4_HUMAN
16	130	8.3	857	1	NEM_CHICK
17	128.5	8.2	731	1	MR11_COPCI
18	127.5	8.2	607	1	KMLC_RABIT
19	127	8.1	3164	1	TEG0_HSV11
20	126.5	8.1	320	1	HXNA_HUMAN
21	126.5	8.1	561	1	3BP2_HUMAN
22	126.5	8.1	628	1	V70K_TYMYA
23	126.5	8.1	1298	1	ICP4_HSV11
24	125.5	8.0	252	1	ICP3_HSV11
25	125	8.0	239	1	NEUM_BOVIN
26	124.5	8.0	217	1	YKRA_EBV
27	124.5	8.0	226	1	BASP_HUMAN
28	124	7.9	1163	1	RTM4_RAT
29	123.5	7.8	1001	1	IF2_SYNY3
30	122.5	7.8	1217	1	APF_MOUSE
31	122	7.8	428	1	APF_MOUSE
32	122	7.8	704	1	NP14_RAT
33	122	7.8	1575	1	SVJ1_HUMAN

34	121.5	7.8	924	1	104K_THEPA
35	121.5	7.8	1083	1	T2D3_HUMAN
36	120.5	7.7	699	1	NP14_HUMAN
37	120	7.7	761	1	TIE2_BRARE
38	120	7.7	1418	1	CA12_HUMAN
39	119.5	7.7	309	1	HXNA_CHICK
40	119	7.6	825	1	ICP0_HSV2H
41	118	7.6	1459	1	CA12_MOUSE
42	117	7.5	314	1	PMXB_HUMAN
43	117	7.5	314	1	PMXB_MOUSE
44	117	7.5	431	1	UL61_HCMVA
45	117	7.5	512	1	IE63_HSV11
					P15711 theileria p
					O00268 homo sapien
					O14978 homo sapien
					O13166 brachydanio
					P02458 homo sapien
					P17277 gallus galli
					P28284 herpes simp
					P28481 mus musculu
					O94453 homo sapien
					O35690 mus musculu
					P16818 human cytom
					P10238 herpes simp

ALIGNMENTS

RESULT 1	UL49_HSV11	STANDARD:	PRT:	301 AA.
ID	UL49_HSV11			
AC	P10233:			
DT	01-MAR-1989 (rel. 10, Created)			
DT	01-MAR-1989 (rel. 10, Last sequence update)			
DT	01-DEC-1992 (rel. 24, Last annotation update)			
DE	Tegument protein UL49.			
GN	UL49.			
OS	Herpes simplex virus (type 1 / strain 17).			
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;			
OC	Alphaherpesvirinae; Simplexvirus.			
OX	NCBI_TaxID=10299;			
RN	[1]			
RA	SEQUENCE FROM N.A.			
RX	MEDLINE=86274327; PubMed=2639594;			
RA	McGoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,			
RT	McNab D., Perry L.J., Scott J.E., Taylor P.			
RT	"The complete DNA sequence of the long unique region in the genome of			
RL	herpes simplex virus type 1."			
J. Gen. Virol.	69:1531-1574(1988).			
CC	!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL49,			
CC	EHV-1 I1, AND VZV 9.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: D10879; BAA01695.1; -			
DR	EMBL: X14112; CAA32299.1; -			
DR	PIR: D30089; WMBE9.			
SO	SEQUENCE 301 AA; 32254 MW; 6E9539C2AE13E29 CRC64;			
Query Match	100.0%; Score 1561; DB 1; Length 301;			
Best Local Similarity	100.0%; Pred. No. 3e-82;			
Matches 301; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
OY	1 MTSRSRVKSGPREVPRDEYEDLYTPSSGMASSPDPSTRGALQTRRORGEVFFVOY 60			
DB	1 MTSRSRVKSGPREVPRDEYEDLYTPSSGMASSPDPSTRGALQTRRORGEVFFVOY 60			
OY	61 DESDVALYGGSSSEDEHPEVPRTRRPVGAVALSGPARAPPPPGSGAGRTPTTAA 120			
DB	61 DESDVALYGGSSSEDEHPEVPRTRRPVGAVALSGPARAPPPPGSGAGRTPTTAA 120			
OY	121 APTQVARKAARAFAETTRGRKSNQPSAALPAPAPATAPTRSTPAQGLARKLHFST 180			
DB	121 APTQVARKAARAFAETTRGRKSNQPSAALPAPAPATAPTRSTPAQGLARKLHFST 180			
OY	181 APPNDAPPTPVAGFNKRVFCAVGRILAMHARMAAVALMDMSRPTDEEDLNELGLT 240			
DB	181 APPNDAPPTPVAGFNKRVFCAVGRILAMHARMAAVALMDMSRPTDEEDLNELGLT 240			

```

Db 181 APPNDADWTPRVAEAFNKRVECAAVGRLAAHMAAVALQMDMSRPRTDEDINELLGIT 240
Qy 241 IRTVYCEBKNNLQANRELVPDVDDVDAATATRRGRSAASRTERPRAPARSARRPV 300
Db 241 IRTVYCEBKNNLQANRELVPDVDDVDAATATRRGRSAASRTERPRAPARSARRPV 300
Qy 301 E 301
Db 301 E 301

RESULT 2
UL49_HSVB STANDARD: PRT: 304 AA.
ID UL49_HSVB
AC P28960:
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Tegument protein (Gene 11 protein).
GN 11.
GC Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
CC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_TaxID=31520:
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92295566; PubMed=1318606;
RX Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
RT "The DNA sequence of equine herpesvirus-1.";
RL Virology 189:304-316(1992).
CC -1. SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL49,
CC EHV-1 11, AND VAV 9.
CC -----
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CC -----
DR EMBL: M86664; AAB02446.1; -.
DR PIR: C36796; W2BEA9.
DR QO SEQUENCE 304 AA; 33240 MW; 937CE27366E79879 CRC64;

```

	Query Match	19.4%	Score 303;	DB 1;	Length 304;	
	Best Local Similarity	32.4%;	Pred. No. 5.2e-11;			
	Matches	93;	Conservative	30;	Indels	68; Gaps 11.
Oy	21 DLYPPSSGMA SPDPPDRSGALQTSRNGEVRFO-----YDSGDALYGSSS	73				
	: :	:	: :	: :	: :	
Dd	58 DLYES-----ASPNDKKYTRRG -WSTAHHYDSEIITYTCGDEYDACEVSLIG----	108				
	:	:	: :	: :	: :	
Oy	74 EDDEHEVPRTRRPVAVLSGPG--PARAPPPAGSGAGRTPTTARABRTORVATK	130				
	: : : :	: :	: :	: :	: :	
Dd	109 -----GKLSTNSGNOSPAKAQPPGGAAAA--PEPRVYRTPPTTAAT-	149				
	:	:	: :	: :	: :	
Oy	131 APAAPAETTRGRKSAOPESALPPOAPASTARTRKSTPNQGLAKLHFEATAPNDAAPT	190				
	: :	: :	: :	: :	: :	
Dd	150 -----STTPROQDCAPQRASPG-----VNSTIKSGGLA---FSGTPTKPSQWY	191				
	:	:	: :	: :	: :	
Oy	191 PRVAGFNKRVFCAAVGRLAAMHAMAAYOLMDMSRPRTDEDENELGITITRYVCEGKN	250				
Dd	192 CATHLEFNKNVFCAAVSRVAHAASDASLWMLNPKTKTEDLDRLFKAATITLVCEGAO	251				
Oy	251 LLQRAVELVNPVDVODVDAATATGRSAASRPTEPRRAPARSARR	297				
	: :	: :	: :	: :	: :	
Dd	252 LLEVANSTMTE-----STPDGYAAAGNGYDRRP-RFASRRR	286				
	:	:	: :	: :	: :	

ID	UL49, HSVBC	STANDARD:	PRT:	258 AA.
AC	P30022:			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	Tegument protein UL49 homolog.			
OS	Bovine herpesvirus type 1 (strain Cooper).			
OC	Vituses; dsDNA viruses, no RNA stage; Herpesviridae;			
CC	Alphaherpesvirinae; Varicelloviruses.			
OX	NCBI_TaxID:10323;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RA	Schwayer M., Styger D., Vogt B., Lowery D.E., Simard C.,			
RA	Lapossiere S., Mira V., Vleck C., Pages V.;			
RL	Submitted (SEP-1995) to the EMBL/Genbank/DBJ databases.			
RN	(2)			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=95264482; PubMed=7745736;			
RX	Liang X., Chow B., Li Y., Rago C., Yoo D., Attah-Poku S.,			
RA	Babluk L.A.;			
RT	"Characterization of bovine herpesvirus 1 UL49 homolog gene and			
RT	product: Bovine herpesvirus 1 UL49 homolog is dispensable for virus			
RT	growth.";			
RL	J. Virol. 69:3863-3867(1995).			
RN	(3)			
RP	SEQUENCE OF 1-95 FROM N.A.			
RX	MEDLINE=93303938; PubMed=8391186;			
RA	Liang X., Tang M., Manns B., Babluk L.A., Zamb T.J.;			
RT	"Identification and deletion mutagenesis of the bovine herpesvirus 1			
RT	dutpase gene and a gene homologous to herpes simplex virus UL49.5.";			
RL	Virology 195:42-50(1993).			
RN	(4)			
RP	SEQUENCE OF 64-258 FROM N.A.			
RX	MEDLINE=93012995; PubMed=1327963;			
RA	Carpenter D.E., Mista V.;			
RT	"Sequences of the bovine herpesvirus 1 homologue of herpes simplex			
RT	virus type-1 alpha-trans-inducing factor (UL48).";			
RL	Gene 119:259-263(1992).			
CC	-1- SIMILIARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL49,			
CC	HSV-1 IL1, AND VZV 9.			
CC	-----			
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CC	-----			
DR	EMBL; Z54206; CAA90920.1; -;			
DR	EMBL; U21137; AAA85715.1; -;			
DR	EMBL; Z11610; -; NOT_ANNOTATED_CDS.			
DR	PRT; S24228; S24228.			
FT	DOMAIN 61 91 ALA-RICH.			
SQ	SEQUENCE 258 AA; 26864 MW; 78C5567442E8A161 CRC64;			

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Query Match          17.4%  Score 271.5: DB 1:  Length 258:
Best Local Similarity 31.2%:  Pred. No. 2.7e-09:
Matches 81:  Conservative 25:  Mismatches 109:  Indels 45:  Gaps 8:

QY 61 DESDY-----ALYGSSEDEDEHEPEVETRRPVSGLVSGRGP-----A 99
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 10 DEDDEYSDLWRENSLYDYESGSDHYEELR-----AATSGPEPGRASVRACAS 62
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 100 RAPPDPAGSG-----GAGRT---PTTAPRAPRTQVATKAPAPA-----AETTGKRSKA 146
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 63 AAAVOPARGBDRRAAAAGCTTAAAPAAAAARRSSSRASSRPPRAADDPVLRPATRGSSGCG 122
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 147 QPESALDPAASTAPRTSKTTPAGCLARKLHSTSTAPPPDDAPTRVAVGKFNKRCVCAVQ 206
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 123 AGAAVAVG--PPRPAPPGANAVASG--PPLAESAPAKPKPAKWCQPTAAVNTTICEANA 178
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

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QY 207 RLAAHMAAVALQMDMSRPDEIDNELGTTITVTCCEGKNLLQRLANELVNDPVOD 266
DB 179 LVAAEYARQAQSDPPKSNERLDRMLKSAIRILVCEGSGLLAANDILARAQRP 238
QY 267 VDAATTRGRSAASRPTERP 286
DB 239 AARGSTSGESRLRCRRARP 258

RESULT 4
ID U49_HSV4 STANDARD: PRT: 290 AA.
AC 000039;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Tegument protein (Gene 11 protein).
GN 11 OR B4.
OS Equine herpesvirus type 4 (strain 1942) (EHV-4) (Equine herpesvirus type 1 subtype 2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_TaxID=10333;
RN 11
RP MEDLINE FROM N.A.
RX MEDLINE-91202570; PubMed-1850013;
RA Whitaker G.R., Riggo M.P., Halliburton I.W., Killington R.A., Allen G.P., Meredith D.M.,
"Antigenic and protein sequence homology between VP13/14, a herpes simplex virus type 1 tegument protein, and gp10, a glycoprotein of RT equine herpesvirus 1 and 4.";
RL J. Virol. 65:2320-2326(1991).
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 U49, EHV-1 11, AND VZV 9.
CC -----
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CC
CC EMBL: X17684; CAA35674.1; .
DR PIR: S36706; S36706.
SQ SEQUENCE 290 AA: 31461 MW: BD57CE14436295FC CRC64:

Query Match 17.3%; Score 270.5; DB 1; Length 290;
Best Local Similarity 34.4%; Pred. No. 3.4e-09;
Matches 85; Conservative 18; Mismatches 77; Indels 67; Gaps 11;
QY 60 YVESDYALYGGSSSEDEHEVPRTRRPVSGAVLSGPG---PARAPPPAGSGAGRTPT 116
DB 84 YPACESLVLGG-----GRLSTSHGRSLSPKTPHPK---SAGVTP- 120
QY 117 TAPRAPRTQRVATKAPAPAEETTRGRKSAOPESALPDAPASTATRTKTAQGL--AR 174
DB 121 -----PQRV-----PARAT-----RAAP--SATPPQPCVAAQRTSPGVNSTKSGK 161
QY 175 KLHFTAPRPDAPMTPRVAGFNKRVFCAVGRLLAAMHARMAVALQMDMSRPRTDEDLNE 234
DB 162 SLAFSCPTPKTPKPMYGATHLFNKNVCAAVRAAHHASDAASLAWDLDPKTTNDDLR 221
QY 235 LLGITITRTVCEGKNLLQRLANELVNDPVQVDAATATRGSS---AASRPTERRAPA 290
DB 222 FLKAAAIRLVCEGSKLEMAN-----ATMERSPDGAAAVADIGYDRP- 265
QY 291 RSASRRP 297
DB 266 RLASRRR 272

RESULT 5
ID U49_VZVD STANDARD: PRT: 302 AA.
AC P09372;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Tegument protein (Gene 9 protein).
GN 9.
OS Varicella-zoster virus (strain Dumas) (VZV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_TaxID=103338;
RN 11
RP MEDLINE FROM N.A.
RX MEDLINE-86306657; PubMed-3018124;
RA Davison A.J., Scott J.E.;
"The complete DNA sequence of varicella-zoster virus.";
RL J. Gen. Virol. 67:1759-1816(1986).
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 U49, EHV-1 11, AND VZV 9.
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CC
CC EMBL: X04370; CAA27892.1; .
DR PIR: 127212; WZBE9.
SQ SEQUENCE 302 AA: 32846 MW: 6557FB44CAE76BF2 CRC64:

Query Match 14.4%; Score 225.5; DB 1; Length 302;
Best Local Similarity 26.2%; Pred. No. 1.3e-06;
Matches 89; Conservative 27; Mismatches 107; Indels 117; Gaps 10;
QY 2 TSTRSVKSGP-----REVRDEEDLYTPSSGMA SPDSPPOTSRRGALQ 46
DB 29 TARSRYVGPDPDSDSLGITYTVGADSPSPYADLYFHKKMTPRVHQPNSS----- 82
QY 47 TTSRQGEVRFQYQYDESDVALYGGSSSEDEHEVPRTRRP-----VSGAVLSGPGA 99
DB 83 -----GSEDDPEDIDEVVAARERARLRLHELVDAVYENPLSV 119
QY 100 RAPPPAGSGAGRTPTTAPRAPRTQRVATKAPAPAEETTRGRKSAOPESALPDAPAS 159
DB 120 EXP-----SRSETKNA-----VKPK-----LEDSP-K 141
QY 160 TAPTSKTPAQLARKLHSTAPRPNDAPMTPRVAGFNKRVFCAVGRLLAAMHARMAVQ 219
DB 142 RAPPGGALTAG--RPISTAPKATATSSMCPPTSPYNNKRCVCAVRVAAMQAKAABA 199
QY 220 LMDMSRPRTDEIDNELGTTITRTVTCCEGKNLLQRLANELVNDPVQVDAATATRG 257
DB 200 AMNSNPNNNAEDRLTLGAVITRTYHGLNLQANENADLGBGASVSKRGHNRKTGLQ 259
QY 258 --LVNPDVVQVDAATATGRSAASRPTERRAPAPASASR 295
DB 260 GGMGNEPMYAGVRKPKSRDTDTGTGRTNRSR--ARSASR 297
RESULT 6
ID IE18_PRIVIF STANDARD: PRT: 1461 AA.
AC P11675;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Immediate-early protein IE180.
GN IE.


```

RESULT 8
IE18_PRVKA STANDARD: PRT: 1446 AA.
AC P33479;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Immediate-early protein IE180.
GN IE.
OS Pseudorabies virus (strain Kaplan) (PRV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_TaxID=33703;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91021039; PubMed=2171211;
RA Vleck C., Kozmik Z., Paces V., Schirm S., Schwzyer M.;
RT "Pseudorabies virus immediate-early gene overlaps with an oppositely
RT oriented open reading frame: characterization of their promoter and
RT enhancer regions.";
RL Virology 179:365-377(1990).
CC -1- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE
CC OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING
CC OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.
CC -1- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.
CC -1- PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF
CC PHOSPHORYLATION.
CC -1- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
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CC -----
DR EMBL: M34651; AAA47470.1; -.
DR PIR: A45344; A45344.
KW Early protein; Transcription regulation; Trans-acting factor;
KW DNA-binding; Phosphorylation; Nuclear protein.
FT DOMAIN 347 354 POLY-SER.
FT DOMAIN 379 397 POLY-SER.
SQ SEQUENCE 1446 AA; 148640 MW; 81F43A3DE3DDA068 CRC64;

Query Match 9.8%; Score 153.5; DB 1; Length 1446;
Best Local Similarity 25.1%; Pred. No. 0.068;
Matches 93; Conservative 35; Mismatches 129; Indels 113; Gaps 18;

OY 3 SRRSVKSGPREVPDEYEDLYTTP-----SSGMASDPSPTDSRRGA 44
DB 41 SRRKSSG-----EDLRFPGGLFSDDAEAVALAAGATRRPRP-----SA 86
OY 45 LQTRSGRGEVFVQYDESD-----YALYGGSSSEDEHPEV---PRT- 85
DB 87 QQQQGRGSGEIVLVDEDEDEDEDEPSPAGSPGALHQGS-----EGLHVLGPRRGA 141
OY 86 ---RPVSGAVLISG-----GRAPARP---PPAGSGAGRTPTTAPRAPRTORVATKA 131
DB 142 GSGRPPTPAALAAEAGAPGGRSSPSAPASSSPG--PSAAPRRWSPARGDDPVG 199
OY 132 PAAPAAETTRGKSAQPEAALPDAPASTAPRTSKTPAOGRLKHLFTAPNPDAPTP 191
DB 200 EPGPARPRTPAAPAP--AAVAAPARRGPPASPAAGPV-----SAPGGGAP--- 248
OY 192 RVAGNKRIVCAVGLAMHA-----RMAAVQLMD-----MSRPDEDLNELL 236
DB 249 -SAGDR-----GRHHQHREPLLDDEPAARRLDPRGLGARSVSSNPNNSNTTIV 300
OY 237 GITTTRATVVCESKNLLQANELLVNDPVOD-----VDATATGR---SAASPTTERPAP 289
DB 301 AVETVARGPEDDELGLAGDGAAPRQPRRRRAGEGALRGGRGFFSSSSSGSDSLSP 360

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OY 290 ARSASRRRP 299
DB 361 ARSPSAPRAP 370

RESULT 9
ICP3_HSV1F STANDARD: PRT: 263 AA.
ID ICP3_HSV1F
AC P08353;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Infected cell protein ICP34.5 (Neurovirulence factor ICP34.5).
GN ICP34.5.
OS Herpes simplex virus (type 1 / strain F).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10304;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86115412; PubMed=3003394;
RA Chou J., Roizman B.;
RT "The terminal a sequence of the herpes simplex virus genome contains
RT the promoter of a gene located in the repeat sequences of the L
RT component.";
RL J. Virol. 57:629-637(1986).
RN [2]
RP REVISIONS.
RX MEDLINE=90156494; PubMed=2154589;
RA Chou J., Roizman B.;
RT "The herpes simplex virus 1 gene for ICP34.5, which maps in inverted
RT repeats, is conserved in several limited-passage isolates but not in
RT strain 17syn+.";
RL J. Virol. 64:1014-1020(1990).
CC -1- FUNCTION: NOT KNOWN. HAS A PROFOUND EFFECT ON THE GROWTH OF THE
CC VIRUS IN CENTRAL NERVOUS SYSTEM TISSUE.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC; IN INFECTED CELL.
CC -1- DEVELOPMENTAL STAGE: ACCUMULATES LATE IN INFECTION.
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CC -----
DR EMBL: M12240; AAA45794.1; ALT_SEQ.
DR PIR: A27768; WMBE38.
KW Repeat; Late protein.
FT DOMAIN 161 190
SQ SEQUENCE 263 AA; 27533 MW; F5084106A08ACB1 CRC64;

Query Match 9.1%; Score 142.5; DB 1; Length 263;
Best Local Similarity 25.6%; Pred. No. 0.056;
Matches 75; Conservative 24; Mismatches 125; Indels 69; Gaps 15;

OY 2 TSSRSVKSQPREVPDEYEDLYTTPSSGMAASDPSPTDSRRGALQTRSGRGEVFRVQYD 61
DB 24 TAOQOVTSTPNSPPA-----VNSAPAAAPPPPPASGPPSCSILLNQ-----WLNVP 70
OY 62 ESDYALYGGSSSEDEHPEVPTTR---RPVSGAVLISGPGAPAPPPAGSGGAGRTPT 116
DB 71 ES-----ASDDDDDDDDWDPSPPEPPAPPEARPTAA---PRG-RSPPEAGGCG--GANS 119
OY 117 TAPRAP-----RTORVATKAPARAARETTGRKKSQPEAALPDAPASTA-PTSKTPA 169
DB 120 HPPSRPFLLPPLALRLRLTAENLARLRLRRAGGBOAPPPPTPTPTATPATPATPATPA 179
OY 170 QGLARKLHFSTAPRPNDAPAWTPTRVAGFNKRVCAVGLA--AMHARMAAVQLMDMSRPR 227

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Db 180 -----TPATPATPTPTPARVRFSPHY---RVRHLYWMAAARLRGSM--ARER 223
Oy 228 TDEDLNLGITTIRVTVCEGNLQANELVNPVDVODATAATGRSAS 280
Db 224 ADR-----ARFRRRVAE-----AEAVIPGCGEPARARALRGAGPAN 261

RESULT 10
MK07_MOUSE STANDARD: PRT: 806 AA.
AC 09WVS8:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mitogen-activated protein kinase 7 (EC 2.7.1.-) (Extracellular signal-
  regulated kinase 5) (ERK-5) (BMK1 kinase).
GN MAPK7 OR ERK5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kamakura S., Moriyuchi T., Nishida E.;
RT "Activation of the protein kinase ERK5/BMK1 by receptor tyrosine
RT kinases: Identification and characterization of a signaling pathway to
RT the nucleus.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MEK5 AND ERK5 INTERACT SPECIFICALLY WITH ONE ANOTHER AND
CC NOT WITH MEK1/ERK1 OR MEK2/ERK2 PATHWAYS (BY SIMILARITY).
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- DOMAIN: THE SECOND PROLINE-RICH REGION MAY INTERACT WITH ACTIN
CC TARGETING THE KINASE TO A SPECIFIC LOCATION IN THE CELL.
CC -1- PTM: AUTOPOHSPHORYLATED ON THREONINE AND TYROSINE RESIDUES, WHEN
CC THE C-TERMINAL PART OF THE KINASE, WHICH COULD HAVE A REGULATORY
CC ROLE, IS ABSENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
CC -----
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CC -----
DR EMBL: AB019373; BAA82039.1; -.
DR HSSP: P27703; 2ERK.
DR MGD: MGI:1346347; Mapk7.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002280; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR SMART: SM00220; S_TKc.1.
DR PROSITE: PS01351; MAPK.1.
DR PROSITE: PS01017; PROTEIN_KINASE_ATP.1.
DR PROSITE: PS01018; PROTEIN_KINASE_SF.1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Cell cycle;
KW Phosphorylation.
KW DOMAIN 55 347 PROTEIN KINASE.
FT DOMAIN 434 465 PRO-RICH 1.
FT DOMAIN 521 524 POLY-ARG.
FT DOMAIN 578 700 PRO-RICH 2.
FT NP_BIND 61 69 ATP (BY SIMILARITY).
FT BINDING 84 84 ATP (BY SIMILARITY).
FT ACT_SITE 182 182 BY SIMILARITY.
FT MOD_RES 219 219 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT MOD_RES 221 221 PHOSPHORYLATION (ACTIVATES THE KINASE)

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FT SQ SEQUENCE 806 AA: 87732 MW: E7CC41C4BDE0633 CRC64; (BY SIMILARITY)
Query Match 8.8%; Score 138; DB 1; Length 806;
Best local Similarity 23.8%; Pred. No. 0.29;
Matches 50; Conservative 22; Mismatches 80; Indels 58; Gaps 5;

Oy 29 GMA5PDSPPDTSRRGALQTRSRGQEVRFVQYD-----ESDVALYGGSSS 73
Db 494 GPSAPLEAPEPRKPVTAQGERERERERRRORERAKEREKROERBRKERGACTGCPST 553
Oy 74 EDEHEEVPRTRRPVGAVLSG-----PGPARAPPPPPSGAGRTPTTA 118
Db 554 D-----PLAGLVLTSDNRSLLERTMRAPAPAPAPAPAPAPSSAQPST 601
Oy 119 PRAPRTQVATKAPA-----APAAETTRGRKSAQEPESALPDAASTAPTRSKTPAAGLAR 174
Db 602 PTGPVSGSTGCPLOPPAGSIRPAGSQPCPPPGVPVQVQAGPTAPALQTAPTSLSASQSLVP 661
Oy 175 KL-----HFSTAPPNDAPWTPR 192
Db 662 PSLPGSGAPEVLPRFPSPGPPDPDGLTPQ 691

RESULT 11
RL_HSV2H
ID RL1_HSV2H STANDARD: PRT: 261 AA.
AC P28283;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Neurovirulence factor (ICP34.5).
GN RL1.
OS Herpes simplex virus (type 2 / strain HG52).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10315;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92113549; PubMed-1662697;
RA McGeoch D.J., Cunningham C., McIntyre G., Dolan A.;
RT "Comparative sequence analysis of the long repeat regions and
RT adjoining parts of the long unique regions in the genomes of herpes
RL simplex viruses types 1 and 2.";
RN J. Gen. Virol. 72:3057-3075(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Dolan A.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: D10471; BAA23428.1; -.
DR EMBL: Z86099; CAB06759.1; -.
DR EMBL: Z86099; CAB06706.1; -.
DR PIR: JQ1502; WMBEXE.
KW Repeat.
KW DOMAIN 3 12 2 X 5 AA TANDEM REPEATS OF R-R-R-G-P.
FT REPEAT 3 7
FT REPEAT 8 12
FT DOMAIN 16 31 2 X 8 AA TANDEM REPEATS OF P-R-P-G-A-P-A-
FT REPEAT 16 23 V.
FT REPEAT 24 31
SQ SEQUENCE 261 AA: 27908 MW: 4BBD13AF3D906D71 CRC64;

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Query Match 8.6%; Score 135; DB 1; Length 261;

Best Local Similarity 25.8%; Pred. No. 0.15; Mismatches 108; Indels 116; Gaps 16;

Matches 85; Conservative 21; Mismatches 108; Indels 116; Gaps 16;

QY 1 MTSRSRV-KSGPREVPDEDELYTTPSSGMA SPDSPDTSRGLATOTRSRQ-----51
 DB 1 MSRRRGPRRRGPRRRP-----PGAPVPRPGAPVPRPGALPTADSNVPAVDSG 51
 QY 52 -----RGEVRFQYDESDYALYGSSSEDEDEPEVPRTRRPVSGAVLSGPGP 98
 DB 52 TAVESAPAASSLRLRWLLVPOADDSDADYAG--NDDAEW-----89
 QY 99 ARAAPPAGGAGRTPTTAPRTQVATKAPAAPAAETTRGRKSAOPESALPDAPA 158
 DB 90 --ANSPSEGG-----KAPAPHAAPAAACPPPPRKE--KGPORPLPHIAL-----134
 QY 159 STAPTRSKTPAAGLAR--KLHFTAPPNPDAP-----WTPRVAGFKRVCAYGLRLAA 210
 DB 135 -----RLRTTETYLARLSLRRRRPPASPADAPKVCFSFPRV-----QVRLVA 179
 QY 211 MH--AAMAAVQMDMSPRFDELDNELGTTTRVYCEG-----KNLLQRA 255
 DB 180 WETAALRLARRGSW--ARERADRRFRFR-----RVAAAEAVIGPCLEPEARARARARA 231
 QY 256 NELVNPVVQDDAATATRGSRASRPTER 285
 DB 232 HEDGFP--AEEDAAAAAAGSSAAAGCGRR 259

RESULT 12

TEGU_EBV STANDARD: PRT; 3149 AA.
 AC P03186;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE Large tegument protein.
 GN BPLF1.
 OS Epstein-Barr virus (strain B95-8) (Human herpesvirus 4).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Lymphocryptovirus.
 OX NCBI_TaxID=10377;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84270667; PubMed=6087149;
 RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
 RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
 RA Tuffnell P.S., Barrell B.G.;
 RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
 RL Nature 310:207-211 (1984).
 CC -1- FUNCTION: TEGUMENT PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
 CC EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
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 CC
 DR EMBL: V01555; CAA24839.1; -
 DR PIR: A03747; Q0B88.
 DR PIR: S32993; S32993.
 SQ SEQUENCE 3149 AA; 337954 MW; 3DD0C576587313D8 CRC64;

Query Match 8.6%; Score 134.5; DB 1; Length 3149;
 Best Local Similarity 27.0%; Pred. No. 1.7;
 Matches 62; Conservative 19; Mismatches 94; Indels 55; Gaps 10;

QY 3 SRSVKSQPREVPDEDELYTTPSSGMA SPDSPDTSRGLATOTRSRQGEVRFVQYDE 62
 DB 372 SAAPASSPLFLIP---IPGLGHP--GVAPSTPPRASSGAARQTPKRRKG-----LQDS 422
 QY 63 SDVALYGG-----SSSEDEHPEVPRTRRPVSGAVLSGPGAPAPP-----PAGSGAGR 113
 DB 423 PHKKPTSGRLPLRSTDTEDDQLRTHVPRH----RPFASARLPVPIPIHQSPASP 478
 QY 114 TPTTAP-----RARTQAV-----ATKAPAAAEETTRGRK- 144
 DB 479 TPHPAPVSTIAPSVTPSPRLQIPLPQAAASNPRIPLTPSPSPSTAAAPPTTTLSP 538
 QY 145 ---SAOPESALPDAPASTAPTRSKTPAAGLARKLHFTAPPNPDAPWTP 191
 DB 539 PPTQQPQPSAAP-APSPPLPQQPPTPSAAPASPLLPQQPPEPSAARAP 587

RESULT 13

WS14_HUMAN STANDARD: PRT; 852 AA.
 ID WS14_HUMAN
 AC Q9NP71; Q9BY06; Q9BY05; Q9BY04; Q9BY03; Q9BE48; Q9YZP3;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Williams-Beuren syndrome chromosome region 14 protein (WS basic-helix-
 DE loop-helix leucine zipper protein) (WS-bHLH) (MLX interactor).
 GN WBSCL14 OR MTO.
 OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20241700; PubMed=10780788;
 RA de Luis O., Valero M.C., Perez Jurado L.A.;
 RT "WBSCL14, a putative transcription factor gene deleted in Williams-
 RT Beuren syndrome: complete characterisation of the human gene and the
 RT mouse ortholog.";
 RL Eur. J. Hum. Genet. 8:215-222 (2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4 AND 5).
 RX PubMed=11230181;
 RA Cairo S., Meria G., Urbina F., Ballabio A., Raymond A.;
 RT "WBSCL14, a gene mapping to the Williams-Beuren syndrome deleted
 RT region, is a new member of the MLX transcription factor network.";
 RL Hum. Mol. Genet. 10:617-627 (2001).
 RN [3]
 RP SEQUENCE OF 620-852 FROM N.A. (ISOFORM 4).
 RX MEDLINE=99075645; PubMed=9860302;
 RA Meng X., Lu X., Li Z., Green E.D., Massa H., Trask B.J., Morris C.A.,
 RA Keating M.T.;
 RT "Complete physical map of the common deletion region in Williams
 RT syndrome and identification and characterization of three novel
 RT genes.";
 RL Hum. Genet. 103:590-599 (1998).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 6).
 RC TISSUE=Eye, and Retinoblastoma;
 RC Strausberg R.;
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR. BINDS TO THE CANONICAL AND
 CC NON-CANONICAL E BOX SEQUENCES 5'-CACGCG-3'.
 CC -1- SUBUNIT: BINDS DNA AS A HETERODIMER WITH MLX/TCFL4.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS: 6 ISOFORMS: 1/ALPHA (SHOWN HERE), 2/BETA,
 CC 3/GAMMA, 4/DELTA, 5/EPSILON AND 6; ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, HEART, KIDNEY, CEREBELLUM
 CC AND INTESTINAL TISSUES.
 CC -1- DISEASE: WBSCL14 is found in a chromosome 17q11.23 commonly
 CC deleted region in the Williams-Beuren syndrome, a multisystem
 CC developmental disorder.
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF

TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.

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DR EMBL: AF156673; AAF68176.1; -
DR EMBL: AF156603; AAF68174.1; -
DR EMBL: AF245470; AAK20935.1; -
DR EMBL: AF245471; AAK20936.1; -
DR EMBL: AF245472; AAK20937.1; -
DR EMBL: AF245473; AAK20938.1; -
DR EMBL: AF245474; AAK20939.1; -
DR EMBL: AF056184; AAD28084.1; -
DR EMBL: BC012923; AAH12923.1; -
DR MIM: 605678; -
DR MIM: 194050; -
DR HSSP: P25912; IHL0.
DR InterPro: IPR001092; HLH_dlm.
DR InterPro: IPR003015; HLH_Myc.
DR Pfam: PF00010; HLH_1.
DR SMART: SM00353; HLH_1.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; 1.
DR Transcription regulation; Repressor; Nuclear protein; DNA-binding;
KW Alternative splicing.
FT DOMAIN 387 394 POLY-PRO.
FT DNA_BIND 409 417 BASIC DOMAIN.
FT DOMAIN 648 662 HELIX-LOOP-HELIX MOTIF (POTENTIAL).
FT DOMAIN 688 702 LEUCINE-ZIPPER.
FT DOMAIN 703 724 MISSING (IN ISOFORM 6).
FT VARSPPLIC 176 268 OETVPEPCPEFLPPPTAP -> AVNGCCGCTSAPOCALGL
FT VARSPPLIC 558 575 (IN ISOFORM 5).
FT VARSPPLIC 576 852 MISSING (IN ISOFORM 5).
FT VARSPPLIC 647 648 MISSING (IN ISOFORM 3 AND ISOFORM 4).
FT VARSPPLIC 687 705 MISSING (IN ISOFORM 2 AND ISOFORM 4).
FT VARSPPLIC 814 815 TV -> ST (IN ISOFORM 6).
FT VARSPPLIC 816 852 MISSING (IN ISOFORM 6).
FT CONFLICT 558 558 MISSING (IN REF. 4).
SQ SEQUENCE 852 AA; 93071 MW; D49E3C3D7C0A72EC CRC64;

Query Match 8.6%; Score 133.5; DB 1; Length 852;
Best Local Similarity 22.7%; Pred. No. 0.56; Mismatches 117; Indels 145; Gaps 14;
Matches 85; Conservative 27;

QY 27 SSGMASPDSPDTSR-----RGALQTRSRQGEVRFVQYDESDYALYGGSSSEDEHP 80
Db 332 SSGTLEGEVPPASSAMTHLSGHSRLQARNSCOPGLDSSAFLLSDFLL-----PE 380

QY 81 VPRRR---RVSGAVLSCGPAPAP-----PPRAGSGA----- 111
Db 381 DPKRLRPPLPPVPLLHYPPPAKVPGLPCPPPPPPMAPPTALLQEPLESPRPPTV 440

QY 112 -----GRTPTAPRA--PRTORVATKAP-----AAPAETT 140
Db 441 PPAAGVPLPAPAPFPPTPSVSPAPTPPIELLPLGYSEPAAGFCFSMPKGPAPAPSP 500

QY 141 RGRKSAOPESALPDAAPASTAPTR-----SKTPAOGIARKLHSTP----- 180
Db 501 RQGASAPPTLAPATVAPSTAGNNPCLTQULLTAKEPEQALEPPLVSTLLRSPGPOET 560

QY 181 -----APPNDAPMTPRVAGNKRKVFCAVGRLLAAMARMAAVOVLMDMSRP----- 226
Db 561 VPEPCTFLPPTP-APPPPR-----PPGPATLAPSRPLVKAERLSPAPSGS 609

QY 227 --RTDEDLNELGLGTTIRTVYCEGKNLQANLVLNPDVQDVADVATATGRSAASRPTE 284
Db 610 ERLISGLDLSMPGCGTISVSKVSPPOPLSRG-----RPD-----SNKTE 648

QY 285 RPARAPASRPPRR 298
Db 649 NRRTHISAEQKR 662

RESULT 14
GSRL_HUMAN
ID GSRL_HUMAN STANDARD; PRT; 1509 AA.
AC Q9NZM4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glioma tumor suppressor candidate region gene 1 protein.
GN GLTSCR1.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX MEDLINE=20175430; PubMed=10708517;
RA Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
RA Portler B.P., Ueki K., Billings S., Ramasamy S., Mohrenweiser H.W.,
RA Schellhauser B.W., Louis D.N., Jenkins R.B.;
RT "A transcript map of the chromosome 19q-Arm glioma tumor suppressor
RT region.";
RL Genomics 64:44-50(2000).
CC -!- TISSUE SPECIFICITY: Expressed at moderate levels in heart, brain,
CC placenta, skeletal muscle, and pancreas, and at lower levels in
CC lung, liver, and kidney.
CC -----
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DR EMBL: AF182077; AAF62874.1; -
DR MIM: 605690; -
FT DOMAIN 37 45 POLY-GLY.
FT DOMAIN 884 889 POLY-PRO.
FT DOMAIN 1214 1225 POLY-SER.
FT DOMAIN 1282 1286 POLY-PRO.
FT DOMAIN 1294 1304 POLY-PRO.
SQ SEQUENCE 1509 AA; 152991 MW; 7C5144F443CE6821 CRC64;

Query Match 8.5%; Score 133; DB 1; Length 1509;
Best Local Similarity 28.5%; Pred. No. 1;
Matches 53; Conservative 21; Mismatches 70; Indels 42; Gaps 10;

QY 26 PSSGMA-SPD-----SPDTSRKALQTRSRQGEVRFVQYDESDYALYGGSSSEDEHP 79
Db 615 PSEGLASPEKIVLGGPPSATPTAILQDSIQ-----MFLQERSQDPL-----SAEGRHL 665

QY 80 EVPTRRPVSGAVLSCGPAPAPPP--PAGSG--GAGRTPTAPAPRTORVATKAPAPAP 136
Db 666 SVF-----ASVYSAPRPQADPAPATPVAKGAGLG-----PQAPDSQASPAAPDIPA 713

QY 137 AETTRG---RKSAPESALPDAAPASTAPTRSKTPAOGIARKLHSTAP-----PN 184
Db 714 AAPLKGPGSPSSPFLPHQAPLGDSPHLPSHPTRPSPRPSRPSQSVSRPSEPLHPCPP 773

QY 185 PDAPWT 190
Db 774 PQAPPT 779

RESULT 15
PAK4_HUMAN

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 12:24:26 ; Search time 29.47 Seconds
(without alignments)
1134.483 Million cell updates/sec

Title: US-09-522-278b-12
Perfect score: 1561
Sequence: 1 MTSRSRVKSGPREVPRDEY.....PTRPRAPARSAPRRPVE 301

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 352077

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A-Geneseq_032802:*
2: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
3: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
4: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
5: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*
6: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*
7: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*
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11: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*
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14: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:*
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16: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*
17: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:*
18: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*
19: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*
20: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
21: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*
22: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	179	11.5	37	20	AAW95100
2	179	11.5	37	21	AAV96575
3	179	11.5	37	21	AAV83262
4	179	11.5	37	21	AAV79878
5	179	11.5	37	22	AAE60911
6	166	10.6	34	22	AAE12206
7	117	7.5	20	19	AAW47198
8	108	6.9	20	19	AAW47197
9	106	6.8	20	19	AAW47201
10	103	6.6	20	19	AAW47200
11	103	6.6	20	19	AAW47199

12	100	6.4	20	19	AAW47203	HSV truncated tegu
13	99	6.3	20	19	AAW47202	HSV truncated tegu
14	89	5.7	20	19	AAW47204	HSV truncated tegu
15	73	4.7	20	19	AAW47196	HSV truncated tegu
16	68.5	4.4	48	20	AAW70854	Human zcytor5 epit
17	64	4.1	48	22	ABG04863	Novel human diagno
18	63	4.0	49	19	AAW54048	C. parvum p23 prot
19	62	4.0	50	22	AAW81939	Human haematologic
20	60.5	3.9	48	21	AAW34165	Gene 20 human secr
21	59	3.8	35	19	AAW70114	Peptide produced b
22	59	3.8	35	22	AAE05575	N-terminal CT6 gly
23	59	3.8	45	21	AAW35605	Arabidopsis thalia
24	59	3.8	46	21	AAW9907	Peptide encoded by
25	58	3.7	30	22	AAW64997	Human brain expres
26	58	3.7	30	22	AAW77718	Human bone marrow
27	58	3.7	30	22	AAW37936	Peptide #11973 enc
28	58	3.7	48	17	AAW95141	Collagen like prot
29	58	3.7	48	22	AAW72766	Repetitive protein
30	58	3.7	48	22	AAW64036	CLP-F functional p
31	57.5	3.7	50	22	AAW42037	Propionibacterium
32	57	3.7	42	20	AAW42511	Collagen type I-de
33	57	3.7	49	22	AAO10627	Human polypeptide
34	57	3.7	50	22	AAW81875	Human haematologic
35	56.5	3.6	50	22	ABG28246	Novel human diagno
36	56	3.6	46	22	AAW63400	Human breast cance
37	55.5	3.6	26	20	AAW70855	Human zcytor5 epit
38	55	3.5	34	22	AAW85615	Monoclonal antibod
39	55	3.5	39	19	AAW44934	Mycobacterial hepa
40	55	3.5	40	22	AAW6933	Human colon cancer
41	54.5	3.5	34	19	AAW48443	Human p53 proline-
42	54.5	3.5	34	22	AAW64409	Human reproductive
43	54.5	3.5	36	21	AAW92847	Human osteoprotegr
44	54.5	3.5	46	14	AAW50053	ICP34.5 fragment.
45	54	3.5	41	22	AAW02061	Human polypeptide

ALIGNMENTS

RESULT 1	AAW95100	standard; peptide: 37 AA.
ID	AAW95100	standard; peptide: 37 AA.
XX	AAW95100;	
XX	25-MAY-1999	(first entry)
XX	HIV-1 VP22 polypeptide C-terminal domain.	
DE		
XX	Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;	
KW	CDK-binding motif; endothelialisation; fusion protein; therapeutic; gene;	
KW	Intracellular; transcytosis; vasculature; wound; repair; hair;	
KW	smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;	
KW	cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;	
KW	tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;	
KW	tachycardia; HIV-1.	
OS	Human immunodeficiency virus type 1.	
XX		
PM	WO9906540-A2.	
XX		
PD	11-FEB-1999.	
XX		
XX	29-JUL-1998;	98WO-US15759.
PR	29-JUL-1997;	97US-0902572.
XX		
PA	(MITO-) MITOXIX INC.	
XX		
PI	Beach DH, Gyuris J, Lamphere L;	
XX		
DR	WPI; 1999-153770/13.	
DR	N-PSDB; AAX26228.	

XX Fusion and chimaeric proteins including cyclin-dependent kinase
 PT binding motif - used for regulation of cell proliferation and
 PT differentiation, for treatment of, e.g. vascular injury, cancers,
 PT fibrosis and neurodegeneration
 XX
 PS Example 2: Page 27: 88pp: English.
 XX
 CC The invention relates to novel inhibitors of cyclin-dependent kinases
 CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
 CC transfection system (A) that comprises: (i) first gene construct
 CC comprising a sequence encoding an inhibitory polypeptide containing at
 CC least one CDK-binding motif for binding and inhibiting activity of a
 CC CDK, linked to a transcription regulator functional in eukaryotic cells;
 CC (ii) second gene construct comprising a sequence encoding a polypeptide
 CC that promotes endothelialisation, and (iii) a gene delivery composition
 CC for delivering the GCS to a cell for transfection. Also provided are
 CC nucleic acids encoding a fusion protein (FP) containing: (i) a
 CC therapeutic polypeptide sequence (TP) from an intracellular protein that
 CC alters a cellular process when FP enters the cell, and (ii) a
 CC transcellular polypeptide sequence (TCP) that promotes transcytosis of
 CC FP. The FP consists of at least one CDK-binding motif and a TCP. See
 CC AAX26220 for detailed uses of the recombinant transfection system. The
 CC CKI polypeptides are engineered to include any of the peptides shown in
 CC AAW5097-100 encoded by the DNA sequences AAX26225-228.
 XX
 SQ Sequence 37 AA:
 Query Match 11.5%: Score 179; DB 20: Length 37;
 Best Local Similarity 100.0%: Pred. No. 4.4e-08;
 Matches 36: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 266 DVDATATGRGSAASRPTERRPARASASRRPRPVE 301
 DB 2 dvdaatatgrgsaasrpterrparasaarprpve 37
 ||||||||||||||||||||||||||||||||||||
 RESULT 2
 AAY96575
 ID AAY96575 standard; Protein: 37 AA.
 XX
 AC AAY96575:
 XX
 DT 12-SEP-2000 (first entry)
 XX
 DE HSV-1 VP22 polypeptide C-terminal domain.
 XX
 KW hESR2; telomerase; catalytic subunit; reverse transcriptase; life-span;
 KW retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;
 KW proliferation; immortal; tumour therapy; macular degeneration; activator;
 KW INK4; HSV-1; VP22; fusion protein.
 XX
 OS Herpes simplex virus 1.
 XX
 PN WO200031238-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 24-NOV-1999; 99WO-US27907.
 XX
 PR 25-NOV-1998; 98US-0109891.
 PR 17-FEB-1999; 99US-0120549.
 XX
 PA (GENE-) GENETICA INC.
 XX
 PI Hannon GJ, Beach DH;
 XX
 DR WPI: 2000-400055/34.
 DR N-PSDB: AAA29396.
 XX
 PT New method for increasing the proliferative capacity of cell lines
 PT comprising administering agents reversibly activating telomerase

PT activity and reversibly inactivating Rb/INK4 and/or p53 pathways useful
 PT in treating age related diseases
 XX
 PS Disclosure: Page 32: 123pp: English.
 XX
 CC The HSV-1 VP22 polypeptide can be fused to a retinoblastoma (Rb)
 CC inactivator protein sequence to aid targeting and internalization.
 CC The invention concerns methods and reagents for extending the life-span,
 CC e.g. the number of mitotic divisions, of a cell. The method relies on
 CC activation of a telomerase activity and inhibition of one or both of a
 CC Rb/INK4 pathway or a p53 pathway. Phosphorylation of Rb by
 CC cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the
 CC division cycle. Binding of INK4 family members, e.g. the tumour
 CC suppressor p16INK4a, inhibits kinase activity and results in growth
 CC arrest. Rb inactivators can selectively and reversibly inactivate an
 CC Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MDM2
 CC is a cellular inhibitor of Rb/E2F function and the p53 tumour suppressor
 CC can also be used in the methods. Other molecules which can be used
 CC include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which
 CC differs from at one or more of residues K22, R24, H95 and/or D97.
 CC Additional constructs include a papilloma virus E7 protein, or other
 CC viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of
 CC the Rb and p16INK4a genes may also be used. The methods are useful for
 CC increasing the proliferative capacity of cells. The cells are
 CC subsequently of use in pharmaceutical and cosmetic preparations used to
 CC treat conditions related to (premature) ageing, e.g. macular degeneration
 CC and arteriosclerosis. The cells can also be used to replace tumour cell
 CC lines in vitro and for studies on biochemical and physiological aspects
 CC of growth and differentiation. Long lived (immortal) cells could also be
 CC of use in the production of normal or genetically engineered
 CC biotechnology products.
 XX
 SQ Sequence 37 AA:
 Query Match 11.5%: Score 179; DB 21: Length 37;
 Best Local Similarity 100.0%: Pred. No. 4.4e-08;
 Matches 36: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 266 DVDATATGRGSAASRPTERRPARASASRRPRPVE 301
 DB 2 dvdaatatgrgsaasrpterrparasaarprpve 37
 ||||||||||||||||||||||||||||||||||||
 RESULT 3
 AAY83262
 ID AAY83262 standard; Protein: 37 AA.
 XX
 AC AAY83262:
 XX
 DT 16-AUG-2000 (first entry)
 XX
 DE HSV-1 V22 C-terminal peptide.
 XX
 KW ubiquitin ligase; SCF; F-box protein; targeted degradation;
 KW destabilisation; proteolysis; drug discovery; gene therapy; cancer;
 KW oncoprotein; Huntington's disease; gene knockout; delivery systems.
 XX
 OS Synthetic.
 XX
 PN WO200022110-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 08-OCT-1999; 99WO-US23705.
 XX
 PR 09-OCT-1998; 98US-0103787.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Zhou P, Howley P;
 XX

DR WPI; 2000-317970/27.
 DR N-PSDB; AA293718.
 XX
 PT Targeting degradation of polypeptide useful for treating cancer and
 PT other proliferative disorders, involves conjugating polypeptide with
 PT ubiquitin protein ligase or inhibiting ubiquitination using organic
 PT compound
 XX
 PS Disclosure; Page 76; 185pp; English.
 XX
 CC The E-box proteins are a family of ubiquitin ligases (SCF ubiquitin
 CC ligases) which can be used for the targeted degradation of a target
 CC polypeptide in vivo. Targeted degradation is achieved by expressing
 CC the ubiquitin ligase in a cell linked to the interaction domain of
 CC the target polypeptide and thereby recruiting the target polypeptide
 CC to the ubiquitin ligase. Such methods are useful for decreasing or
 CC increasing the level of a target polypeptide and for creating and
 CC expressing a destabilized polypeptide which is subjected to SCF
 CC mediated proteolysis. Degrading any desired protein in a cell is
 CC useful for preventing or treating diseases caused by the presence of
 CC abnormal amount of the specific polypeptides, for drug discovery and
 CC for gene therapy. Diseases treated include cancer, by degradation of
 CC oncoproteins, Huntington's disease, other proliferative disorders and
 CC microbial infections. The method provides a quick and easy
 CC alternative to gene knockout technology. The target polypeptide can
 CC be degraded at all stages, or a specific stage, of development in the
 CC mature animal. The hybrid ubiquitin ligase may also include an
 CC optional localisation sequence such as this HSV-1 V22 sequence.
 XX
 SQ Sequence 37 AA:
 Query Match 11.5%; Score 179; DB 21; Length 37;
 Best Local Similarity 100.0%; Pred. NO. 4.4e-08;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 266 DVDAAATATGRSAASRPTERRPAPASASRRPVE 301
 DB 2 dvdaatatgrsaasrpterrpapasasrrpve 37
 ID AAV79878 standard; Peptide; 37 AA.
 AC AAV79878;
 XX
 DT 10-MAY-2000 (first entry)
 XX
 DE HSV-1 VP22 C-terminal domain peptide.
 XX
 KM Papillomavirus; PV; infection; cell proliferation; E2; peptidomimetic;
 KM EL; antiviral; virucide; cytostatic; antiproliferative; dermatological;
 KM preneoplastic lesion; neoplastic lesion; cutaneous lesion; wart;
 KM epidermodysplasia verruciformis; anorectal carcinoma.
 XX
 OS Herpes simplex virus type 1.
 XX
 PM WO200001720-A2.
 XX
 PD 13-JAN-2000.
 XX
 PF 02-JUL-1999; 99WO-US15144.
 XX
 PR 02-JUL-1998; 98US-0091661.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Howley P, Benson J, Kasukawa H;
 XX
 DR WPI; 2000-171001/15.
 DR N-PSDB; AA288469.
 XX

PT Use of papillomavirus E2 protein peptidomimetics for treating
 PT papillomavirus-infected cells and papillomavirus-induced conditions in
 PT mammals by inhibiting E1-E2 interaction
 XX
 PS Disclosure; Page 43; 110pp; English.
 XX
 CC The present invention describes the use of a small organic compound (A)
 CC which competitively inhibits interaction of a papillomavirus (PV) E2
 CC protein with a PV E1 protein for treating a cell infected with PV or a
 CC mammal with a PV-induced condition. (A) has antiviral, virucide,
 CC cytostatic, antiproliferative and dermatological activities. Methods
 CC from the present invention can be used to treat PV-induced conditions
 CC including growth of PV preneoplastic and neoplastic lesions, cutaneous
 CC lesions chosen from warts and other benign cutaneous lesions, plantar
 CC warts (verruca plantaris), common warts (verruca plana), Butcher's
 CC common warts, flat warts, genital warts (condyloia acuminatum) and
 CC epidermodysplasia verruciformis, laryngeal, oral, pharyngeal,
 CC oesophageal and other upper airway papilloma or vaginal, cervical,
 CC vulvar, penile and anorectal carcinoma. The E2 inhibitors may also be
 CC used to treat epithelial and internal fibropapillomas in animals.
 CC The present sequence represents a peptide sequence used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 37 AA:
 Query Match 11.5%; Score 179; DB 21; Length 37;
 Best Local Similarity 100.0%; Pred. NO. 4.4e-08;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 266 DVDAAATATGRSAASRPTERRPAPASASRRPVE 301
 DB 2 dvdaatatgrsaasrpterrpapasasrrpve 37
 ID AAB60911 standard; Peptide; 37 AA.
 AC AAB60911;
 XX
 DT 05-NOV-2001 (first entry)
 XX
 DE HSV-1 VP22 C-terminus.
 XX
 KM Co-activator domain; P300/CBP KIX domain; erythrocythaemia; skin disease;
 KM polycythaemia; haemoglobinopathy; cell differentiation; ulcer; cancer;
 KM neurological condition; neurodegenerative disease; immune disease;
 KM diabetes.
 XX
 OS Synthetic.
 XX
 PM WO200118036-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 31-AUG-2000; 2000WO-US24010.
 XX
 PR 03-SEP-1999; 99US-0152402.
 XX
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 PA (JOSL-) JOSLIN DIABETES CENT INC.
 XX
 PI Frangioni JV, Cantley LC, Montminy MR;
 XX
 DR WPI; 2001-273380/28.
 DR N-PSDB; AAF58997.
 XX
 PT Identifying co-activator domain specific transcriptional activators by
 PT contacting a target domain of a selected transcription factor with a
 PT peptide display library, where the identified binding peptides are
 XX useful for reducing hyperglycemia -

PS Disclosure; page 79; 156pp; English.

XX The present invention describes a method of identifying the co-activator
 CC domain of specific synthetic activators, involving contacting the target
 CC domain of a selected transcription factor with a peptide display library,
 CC and identifying those sequences which bind to the target domain. In
 CC particular, those which bind to the KIX domain of p300/CBP are useful.
 CC The peptides can be used in the treatment of diseases related to aberrant
 CC KIX-dependent gene transcription, including erythrocythemia,
 CC polycythemia, haemoglobinopathies, to regulate cell differentiation, to
 CC treat neurological diseases, immunological diseases, diabetes, ulcers,
 CC skin diseases and cancer, and to aid wound healing. The present sequence
 CC is a peptide described in the exemplification of the invention.

XX Sequence 37 AA:

Query Match 11.5%; Score 179; DB 22; Length 37;
 Best Local Similarity 100.0%; Pred. No. 4.4e-08;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 266 DVDAATATRCRSASRPTERRAPARSASRRPVE 301
 |||||||||||||||||||||||||||||||||
 DB 2 dvdaataatrgrsaasrpterraparsasrrpve 37

RESULT 6
 AAE12206
 ID AAE12206 standard; peptide; 34 AA.

XX AAE12206;

XX 18-DEC-2001 (first entry)

DE Membrane transport sequence of herpes simplex virus type 1.

XX

KW Polyglutamine repeat domain; huntingtin; atrophin; ataxin;
 KW androgen receptor protein; neurodegenerative disease; anticonvulsant;
 KW Huntington's disease; dentatorubral pallidoluysian atrophy; DRPLA;
 KW spinobulbar muscular atrophy; spinocerebellar ataxia; noctropic;
 KW membrane transport sequence.

XX

OS Herpes simplex virus type 1.

XX

PN WO200168678-A2.

XX

PD 20-SEP-2001.

XX

PF 14-MAR-2001; 2001WO-US08222.

XX

PR 16-MAR-2000; 2000US-189781P.

XX

PA (UYDU-) UNITV DUKE.

XX

PI Strittmatter WJ, Burke JR, Nagai Y;

XX

DR WPI: 2001-616285/71.

XX

PT New polypeptides which selectively bind to expanded polyglutamine
 PT repeat domains, useful for treating neurodegenerative diseases, e.g.
 PT Huntington's disease -

XX

XX Example 14; Page 59; 59pp; English.

XX The present sequence is a membrane transport sequence of
 CC herpes simplex virus type 1 which is fused to the polyglutamine binding
 CC peptide. The peptide is useful for treating a cell that contains and
 CC expresses a protein having an expanded polyglutamine region (e.g.
 CC huntingtin; atrophin 1, ataxin 1, 2, 6 or 7; or androgen receptor
 CC protein), or treating a neurodegenerative disease characterised by the
 CC presence of expanded polyglutamine repeats, e.g. Huntington's disease,
 CC dentatorubral pallidoluysian atrophy (DRPLA), spinobulbar muscular
 CC atrophy, and spinocerebellar ataxia types 1, 2, 3, 6 and 7.

XX Sequence 34 AA;

SQ

Query Match 10.6%; Score 166; DB 22; Length 34;
 Best Local Similarity 97.1%; Pred. No. 4.7e-07;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 268 DAATATRCRSASRPTERRAPARSASRRPVE 301
 |||||||||||||||||||||||||||||||||
 DB 1 daataatrgrsaasrpterraparsasrrpve 34

RESULT 7
 AAM47198
 ID AAM47198 standard; peptide; 20 AA.

XX AAM47198;

XX 03-JUL-1998 (first entry)

DE HSV truncated tegument protein VP22 derived peptide C.

XX

KW HSV, tegument protein; VP22; UL49; antiviral agent; treatment;
 KW cold sore; genital herpes; chickenpox; shingles.

XX

OS Herpes simplex virus.

XX

OS Synthetic.

XX

PN WO9804708-A1.

XX

PD 05-FEB-1998.

XX

PF 28-JUL-1997; 97WO-GB02036.

XX

PR 26-JUL-1996; 96GB-0015726.

XX

PA (MED-) MEDICAL RES COUNCIL.

XX

PI Hope RG, McGeoch DJ, McLaughlan J, Rixon HM;

XX

DR WPI: 1998-130696/12.

XX

PT New antiviral agent disrupting binding of VP22 to VP16 or gB -
 PT useful for treating infections caused by herpes simplex, e.g. cold
 PT sores and chicken-pox

XX

PS Example; Page 25; 75pp; English.

XX

CC The present sequence is a herpes simplex virus (HSV) truncated
 CC tegument protein VP22 derived peptide. VP22 was used in the
 CC preparation of a novel antiviral agent, which inhibits the
 CC maturation and/or replication of HSV by disrupting association
 CC between VP22 and VP16 and/or gB. The agent can be used to treat,
 CC e.g. cold sores, genital herpes, chickenpox and shingles.

XX

SQ Sequence 20 AA;

Query Match 7.5%; Score 117; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 178 FSTAPPNDAPWTPRVAGFN 197
 |||||||||||||||||||
 DB 1 fstappndapwtprvagfn 20

RESULT 8
 AAM47197
 ID AAM47197 standard; peptide; 20 AA.

XX

AC AAM47197;

```
XX 03-JUL-1998 (first entry)
DE HSV truncated tegument protein VP22 derived peptide B.
XX
XX HSV, tegument protein; VP22; UL49; antiviral agent; treatment;
KM cold sore; genital herpes; chickenpox; shingles.
XX
OS Herpes simplex virus.
XX Synthetic.
XX
XX WO9804708-A1.
XX
XX 05-FEB-1998.
XX
XX 28-JUL-1997; 97WO-GB02036.
XX
XX 26-JUL-1996; 96GB-0015726.
XX
XX (MEDI-) MEDICAL RES COUNCIL.
XX
XX Hope RG, McGeoch DJ, McLaughlan J, Rixon HM.
XX
XX WPI; 1998-130696/12.
XX
XX New antiviral agent disrupting binding of VP22 to VP16 or gB -
XX useful for treating infections caused by herpes simplex, e.g. cold
XX sores and chicken-pox
XX
XX Example; Page 25; 75pp; English.
XX
XX The present sequence is a herpes simplex virus (HSV) truncated
XX tegument protein VP22 derived peptide. VP22 was used in the
XX preparation of a novel antiviral agent, which inhibits the
XX maturation and/or replication of HSV by disrupting association
XX between VP22 and VP16 and/or gB. The agent can be used to treat,
XX e.g. cold sores, genital herpes, chickenpox and shingles.
XX
XX Sequence 20 AA:
SQ
Query Match 6.9%; Score 108; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 166 KTPAGGLARKLHSTAPPNP 185
Db 1 ktpagglarklhfstappnp 20
RESULT 9
AAW47201
ID AAW47201 standard; peptide; 20 AA.
XX
XX AAW47201;
AC
XX
XX 03-JUL-1998 (first entry)
DE HSV truncated tegument protein VP22 derived peptide F.
XX
XX HSV, tegument protein; VP22; UL49; antiviral agent; treatment;
KM cold sore; genital herpes; chickenpox; shingles.
XX
OS Herpes simplex virus.
XX Synthetic.
XX
XX WO9804708-A1.
XX
XX 05-FEB-1998.
XX
XX 28-JUL-1997; 97WO-GB02036.
XX
XX 26-JUL-1996; 96GB-0015726.
XX
```

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XX (MEDI-) MEDICAL RES COUNCIL.
XX
XX Hope RG, McGeoch DJ, McLaughlan J, Rixon HM.
XX
XX WPI; 1998-130696/12.
XX
XX New antiviral agent disrupting binding of VP22 to VP16 or gB -
XX useful for treating infections caused by herpes simplex, e.g. cold
XX sores and chicken-pox
XX
XX Example; Page 25; 75pp; English.
XX
XX The present sequence is a herpes simplex virus (HSV) truncated
XX tegument protein VP22 derived peptide. VP22 was used in the
XX preparation of a novel antiviral agent, which inhibits the
XX maturation and/or replication of HSV by disrupting association
XX between VP22 and VP16 and/or gB. The agent can be used to treat,
XX e.g. cold sores, genital herpes, chickenpox and shingles.
XX
XX Sequence 20 AA:
SQ
Query Match 6.8%; Score 106; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 214 RMAAVQLMDMSRPRTDEDIN 233
Db 1 rmaavqlwmsrptdedin 20
RESULT 10
AAW47200
ID AAW47200 standard; peptide; 20 AA.
XX
XX AAW47200;
AC
XX
XX 03-JUL-1998 (first entry)
DE HSV truncated tegument protein VP22 derived peptide E.
XX
XX HSV, tegument protein; VP22; UL49; antiviral agent; treatment;
KM cold sore; genital herpes; chickenpox; shingles.
XX
OS Herpes simplex virus.
XX Synthetic.
XX
XX WO9804708-A1.
XX
XX 05-FEB-1998.
XX
XX 28-JUL-1997; 97WO-GB02036.
XX
XX 26-JUL-1996; 96GB-0015726.
XX
XX (MEDI-) MEDICAL RES COUNCIL.
XX
XX Hope RG, McGeoch DJ, McLaughlan J, Rixon HM.
XX
XX WPI; 1998-130696/12.
XX
XX New antiviral agent disrupting binding of VP22 to VP16 or gB -
XX useful for treating infections caused by herpes simplex, e.g. cold
XX sores and chicken-pox
XX
XX Claim 10; Page 25; 75pp; English.
XX
XX The present sequence is a herpes simplex virus (HSV) truncated
XX tegument protein VP22 derived peptide. VP22 was used in the
XX preparation of a novel antiviral agent, which inhibits the
XX maturation and/or replication of HSV by disrupting association
XX between VP22 and VP16 and/or gB. The agent can be used to treat,
```

CC e.g. cold sores, genital herpes, chickenpox and shingles.
 XX
 SQ Sequence 20 AA;

Query Match 6.6%; Score 103; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 202 CAVGRLAAMHARMAAVQLM 221
 ||||||||||||||||
 Db 1 caavgrlaamharmaavqlm 20

RESULT 11
 AAM47199
 ID AAM47199 standard; peptide; 20 AA.
 XX
 AC AAM47199;

XX 03-JUL-1998 (first entry)
 XX
 DE HSV truncated tegument protein VP22 derived peptide D.
 XX
 KW HSV; tegument protein; VP22; UL49; antiviral agent; treatment;
 KM cold sore; genital herpes; chickenpox; shingles.
 XX
 OS Herpes simplex virus.
 OS Synthetic.
 XX
 PN WO9804708-A1.
 XX
 PD 05-FEB-1998.
 XX
 PF 28-JUL-1997; 97WO-GB02036.
 XX
 PR 26-JUL-1996; 96GB-0015726.
 XX
 PA (MEDI-) MEDICAL RES COUNCIL.
 XX
 PI Hope RG, McGeoch DJ, McLaughlan J, Rixon HM;

XX WPI; 1998-130696/12.
 XX
 PT New antiviral agent disrupting binding of VP22 to VP16 or gB -
 PT useful for treating infections caused by herpes simplex, e.g. cold
 PT sores and chicken-pox
 XX
 PS Claim 5; Page 25; 75pp; English.
 XX
 CC The present sequence is a herpes simplex virus (HSV) truncated
 CC tegument protein VP22 derived peptide. VP22 was used in the
 CC preparation of a novel antiviral agent, which inhibits the
 CC maturation and/or replication of HSV by disrupting association
 CC between VP22 and VP16 and/or gB. The agent can be used to treat,
 CC e.g. cold sores, genital herpes, chickenpox and shingles.
 XX
 SQ Sequence 20 AA;

Query Match 6.6%; Score 103; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 190 TPRVAGFNKRVCFAVGRLA 209
 ||||||||||||||||
 Db 1 tprvagfnkrvcfaavgrla 20

RESULT 12
 AAM47203
 ID AAM47203 standard; peptide; 20 AA.
 XX

AC AAM47203;
 XX
 DT 03-JUL-1998 (first entry)
 XX
 DE HSV truncated tegument protein VP22 derived peptide H.
 XX
 KW HSV; tegument protein; VP22; UL49; antiviral agent; treatment;
 KM cold sore; genital herpes; chickenpox; shingles.
 XX
 OS Herpes simplex virus.
 OS Synthetic.
 XX
 PN WO9804708-A1.
 XX
 PD 05-FEB-1998.
 XX
 PF 28-JUL-1997; 97WO-GB02036.
 XX
 PR 26-JUL-1996; 96GB-0015726.
 XX
 PA (MEDI-) MEDICAL RES COUNCIL.
 XX
 PI Hope RG, McGeoch DJ, McLaughlan J, Rixon HM;

XX WPI; 1998-130696/12.
 XX
 PT New antiviral agent disrupting binding of VP22 to VP16 or gB -
 PT useful for treating infections caused by herpes simplex, e.g. cold
 PT sores and chicken-pox
 XX
 PS Claim 5; Page 25; 75pp; English.
 XX
 CC The present sequence is a herpes simplex virus (HSV) truncated
 CC tegument protein VP22 derived peptide. VP22 was used in the
 CC preparation of a novel antiviral agent, which inhibits the
 CC maturation and/or replication of HSV by disrupting association
 CC between VP22 and VP16 and/or gB. The agent can be used to treat,
 CC e.g. cold sores, genital herpes, chickenpox and shingles.
 XX
 SQ Sequence 20 AA;

Query Match 6.4%; Score 100; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.077;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 238 ITTIRVTVCCKNLQRPAN 257
 ||||||||||||||||
 Db 1 ittirvtvccknllqrpne 20

RESULT 13
 AAM47202
 ID AAM47202 standard; peptide; 20 AA.
 XX
 AC AAM47202;

XX 03-JUL-1998 (first entry)
 XX
 DE HSV truncated tegument protein VP22 derived peptide G.
 XX
 KW HSV; tegument protein; VP22; UL49; antiviral agent; treatment;
 KM cold sore; genital herpes; chickenpox; shingles.
 XX
 OS Herpes simplex virus.
 OS Synthetic.
 XX
 PN WO9804708-A1.
 XX
 PD 05-FEB-1998.
 XX
 PF 28-JUL-1997; 97WO-GB02036.
 XX

```

PR 26-JUL-1996: 96GB-0015726.
XX
XX (MEDI-) MEDICAL RES COUNCIL.
XX
PI Hope RG, McGeoch DJ, McLaughlan J, Rixon HMW;
XX
DR WPI: 1998-130696/12.
XX
PT New antiviral agent disrupting binding of VP22 to VP16 or gB -
PT useful for treating infections caused by herpes simplex, e.g. cold
PT sores and chicken-pox
PS
XX Example: Page 25; 75pp; English.
XX
CC The present sequence is a herpes simplex virus (HSV) truncated
CC tegument protein VP22 derived peptide. VP22 was used in the
CC preparation of a novel antiviral agent, which inhibits the
CC maturation and/or replication of HSV by disrupting association
CC between VP22 and VP16 and/or gB. The agent can be used to treat,
CC e.g. cold sores, genital herpes, chickenpox and shingles.
XX
SQ Sequence 20 AA:

```

```

Query Match 6.3%; Score 99; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 226 PRTDDELNLGITTIRTV 245
    |||||
    1 pttedlnellgittirvtv 20
DB

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RESULT 14

```

AAW47204
ID AAW47204 standard; peptide; 20 AA.
XX
XX AAW47204;
XX
XX 03-JUL-1998 (first entry)
XX
DE HSV truncated tegument protein VP22 derived peptide I.
XX
XX HSV; tegument protein; VP22; UL49; antiviral agent; treatment;
XX cold sore; genital herpes; chickenpox; shingles.
XX
OS Herpes simplex virus.
OS Synthetic.
XX
XX MO9804708-A1.
XX
XX 05-FEB-1998.
XX
XX 28-JUL-1997: 97WO-GB02036.
XX
XX 26-JUL-1996: 96GB-0015726.
XX
XX (MEDI-) MEDICAL RES COUNCIL.
XX
XX Hope RG, McGeoch DJ, McLaughlan J, Rixon HMW;
XX
XX WPI: 1998-130696/12.
XX
XX New antiviral agent disrupting binding of VP22 to VP16 or gB -
XX useful for treating infections caused by herpes simplex, e.g. cold
XX sores and chicken-pox
XX
XX Example: Page 25; 75pp; English.
XX
XX The present sequence is a herpes simplex virus (HSV) truncated
XX tegument protein VP22 derived peptide. VP22 was used in the
XX preparation of a novel antiviral agent, which inhibits the
XX maturation and/or replication of HSV by disrupting association
XX between VP22 and VP16 and/or gB. The agent can be used to treat,
XX e.g. cold sores, genital herpes, chickenpox and shingles.
XX
XX Sequence 20 AA:

```

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CC between VP22 and VP16 and/or gB. The agent can be used to treat,
CC e.g. cold sores, genital herpes, chickenpox and shingles.
XX
XX
SQ Sequence 20 AA:

```

```

Query Match 5.7%; Score 89; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 250 NILQRANELVNPVVQDV 267
    |||||
    1 nilqranelvnpvqvqv 18
DB

```

RESULT 15

```

AAW47196
ID AAW47196 standard; peptide; 20 AA.
XX
XX AAW47196;
XX
XX 03-JUL-1998 (first entry)
XX
XX HSV truncated tegument protein VP22 derived peptide A.
XX
XX HSV; tegument protein; VP22; UL49; antiviral agent; treatment;
XX cold sore; genital herpes; chickenpox; shingles.
XX
OS Herpes simplex virus.
OS Synthetic.
XX
XX MO9804708-A1.
XX
XX 05-FEB-1998.
XX
XX 28-JUL-1997: 97WO-GB02036.
XX
XX 26-JUL-1996: 96GB-0015726.
XX
XX (MEDI-) MEDICAL RES COUNCIL.
XX
XX Hope RG, McGeoch DJ, McLaughlan J, Rixon HMW;
XX
XX WPI: 1998-130696/12.
XX
XX New antiviral agent disrupting binding of VP22 to VP16 or gB -
XX useful for treating infections caused by herpes simplex, e.g. cold
XX sores and chicken-pox
XX
XX Example: Page 25; 75pp; English.
XX
XX The present sequence is a herpes simplex virus (HSV) truncated
XX tegument protein VP22 derived peptide. VP22 was used in the
XX preparation of a novel antiviral agent, which inhibits the
XX maturation and/or replication of HSV by disrupting association
XX between VP22 and VP16 and/or gB. The agent can be used to treat,
XX e.g. cold sores, genital herpes, chickenpox and shingles.
XX
XX Sequence 20 AA:

```

```

Query Match 4.7%; Score 73; DB 19; Length 20;
Best Local Similarity 93.8%; Pred. No. 14;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 158 ASTAPTRSKTPAQGLA 173
    |||||
    5 artaptksktpaqgla 20
DB

```

Search completed: August 28, 2002, 12:28:33
Job time: 247 sec

• • • • •

XX WPI: 1999-551046/46.
DR N-PSDB: AA219784.

XX New produg activating agent targeted to selected cells or tissues,
PT particularly hypoxic cells, for treating e.g. tumors -

XX Example 7; Fig 3; 187pp; English.

XX This sequence represents a Herpes simplex virus type 1 (HSV-1)
CC VP22 tegument protein, which is involved in transcellular
CC localisation. VP22 can be fused to cytochrome P450 reductase (P450R)
CC derivatives such as anionless P450R (AA142287) or FN fragment
CC (AA142288). This enables the fusion protein to be delivered to
CC neighbouring cells where it is then transported to the nucleus. Many
CC drugs' sites of action are in the nucleus, rather than the cytoplasm,
CC where P450R normally functions. P450R or its derivatives can be used to
CC activate produgs to their active form via reduction. Administration of a
CC produg is useful where the active drug may be metabolised before it
CC reaches its site of action or where the active drug is cytotoxic, e.g.,
CC anticancer drugs. Targeted delivery of such produg activators allows a
CC reduction in dose of the produg, and thus of systemic side-effects.
CC P450R derivative fusion proteins, or vectors that express them, are
CC specifically used to treat tumours, inflammation, atherosclerosis and
CC muscular dystrophy, but may also be used to treat many other conditions,
CC e.g., cerebral malaria, rheumatoid arthritis, or conditions associated
CC with hypoxia, ischaemia or hypoglycemia, or to deliver antibiotics,
CC antiviral agents, analgesics, anaesthetics, anti-inflammatory,
CC antineoplastic agents and diagnostic agents.

XX Sequence 301 AA:

Query Match 100.0%; Score 1561; DB 20; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.3e-122;
Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSRRSVKSGPREVPDEDELYTPSSGMA SPDPSTSRGALOTRSRORGEVRFVY 60
DB 1 mtsrrsvksqprevpdeyedylytpssgmaspdpdstrgalotrsrqregevfvy 60
QY 61 DESDVALYGGSSSEDEHPEVPTRRPVSGAVLSGPGPARAPPAGSGAGTPTTAPR 120
DB 61 desdvalyggsssedehpevprrtrpvsgavlspgparapppgsgaggtpttapt 120
QY 121 APPTORVATAPAPAPAEETTRGRKSAOPESAAIPDAPASTAPRSTPAAGLARKLHFT 180
DB 121 apttrvatapapapaeetrgrksaqpesaalpdapastaprrstktptagglarklhft 180
QY 181 APPNPDAWTPTRVAGFNKRVFCAVGLAAMHARMAAVQLMDSRPRTDEDLNELLGITT 240
DB 181 appnpdawtptrvagnkrfvcaavglaaamharmavqlmdsrprtdeedlnellgitt 240
QY 241 IRTVCEGKLLORANELVDPVOVDATATRGSAARPRTERPRAPARSRRPRPV 300
DB 241 irtvcegklloranelvdpvovdatatrgsaarprterpraparsrrprpv 300
QY 301 E 301
DB 301 e 301

RESULT 2
AAV27404
ID AAV27404 standard: Protein: 301 AA.

XX AAV27404:

XX 23-NOV-1999 (first entry)

XX HSV-1 tegument protein VP22.

XX Produg: localization domain: tumor-selective antibody; cytochrome P450;

KW produg activating domain; modified hematopoietic stem cell; MHC; tumor;
KW inflammation; atherosclerosis; muscular dystrophy; cerebral malaria;
KW rheumatoid arthritis; hypoxia; ischemia; hypoglycemia; HSV; VP22;
KW tegument protein.

OS Herpes simplex virus type 1.

XX Key Location/Qualifiers
XX Region 251..267

FT /note="the corresponding DNA sequence for this region
FT is possibly missing; there are only 4 nucleotide
FT basepairs indicated as encoding for this entire
FT region"

MO9945126-A2

PD 10-SEP-1999.

XX 05-MAR-1999; 99WO-GB00672.

XX 06-MAR-1998; 98GB-0004841.

XX 19-AUG-1998; 98GB-0018103.

XX 29-JAN-1999; 99GB-0002081.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Stratford IJ, Patterson AV, Kingsman SM, Kan O, Griffiths L;

XX Mitrophanous K;

XX WPI: 1999-540852/45.

XX N-PSDB: AA207807.

XX New produg activating agent targeted to selected cells or tissues,
XX particularly hypoxic cells, for treating e.g. tumors or inflammation -

XX Example 7; Fig 3d; 149pp; English.

XX The invention provides a new produg activating agent that comprises: (1)
CC a localization domain (LD); other than a tumor-selective antibody; and a
CC produg activating domain (PAD); (11) at least one nucleic acid encoding
CC a cytochrome P450 and under control of at least one constitutive or
CC inducible expression control sequence or (11) a modified hematopoietic
CC stem cell (MHC) containing at least one nucleic acid encoding a PAD and
CC under control of elements as in (11). The produg activating agent or
CC vectors that express them, are specifically used to treat tumors,
CC inflammation, atherosclerosis and muscular dystrophy, but may also be
CC used to treat many other conditions, e.g. cerebral malaria, rheumatoid
CC arthritis, or conditions associated with hypoxia, hypoglycemia or
CC ischemia, or to deliver antibiotics, antiviral agents, analgesics,
CC anesthetics, anti-inflammatory, antineoplastic agents and diagnostic
CC agents. LD optimize activity of PAD, e.g. by delivering it to selected
CC locations or by delivering it to neighboring cells (bystander effect),
CC and allow a reduction in dose of produg, and thus of systemic side-
CC effects. Nucleic acids encoding the agent may be expressed selectively
CC in hypoxic cells. The present sequence represents the HSV-1 tegument
CC protein VP22. This is used in the construction of a fusion protein
CC comprising VP22 and a human P450 reductase derivative alp450R.

XX Sequence 301 AA:

Query Match 100.0%; Score 1561; DB 20; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.3e-122;
Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSRRSVKSGPREVPDEDELYTPSSGMA SPDPSTSRGALOTRSRORGEVRFVY 60

DB 1 mtsrrsvksqprevpdeyedylytpssgmaspdpdstrgalotrsrqregevfvy 60

QY 61 DESDVALYGGSSSEDEHPEVPTRRPVSGAVLSGPGPARAPPAGSGAGTPTTAPR 120

DB 61 desdvalyggsssedehpevprrtrpvsgavlspgparapppgsgaggtpttapt 120

OY		1	MTSRRSVKSQGREVPREDIEDLYTTPSSGNASPDSPDTSRRGALQTRSQRGEVRFOY	600
D8		1	MTSRISVSKSGPREVPREDEYEDLYTTPSSGNASPDSPDTSRRGALQTRSGRGEVRFVQY	600

Query Match	100.0%	Score 1561	DB 22	length 301
Best Local Similarity	100.0%	Pred. No. 5.3e-122		

	Matches	301.	Conservative	0:	Mismatches	0;	Indels	0;	Gaps	0;
OY	1	MTSRRSVKS	SQGPREVPREDIEDLYTPSSGMSAPDSPPDTSRRGAIQTRSKRGCEVRFOY	60						
Dd	1	mstrsrsvksqgp	rprevrdeyedilytpssgmsapdsppdstrrrgalqltrsgrgevrivgy	60						
OY	61	DESDVALYGSSSEDDHEHPEPRTRRPVSQAIVLSGGPRAAPPAGSGAARTPTTAR	120							
Dd	61	deshdalylggssseddhpevprtlrtipvsqaivlsggparapppgsgagrcptctapr	120							
OY	121	AFRTQRVTAKPAAPAETTRGRKSAOESALPLPAPASTAPTFRSCTPAOGIARKLHFST	180							
Dd	121	afrtqrvtakpaapaetaetrgrkseaopesaalpldapastaptfrsktpaqgiarklhfst	180							
OY	181	APPNPDAWTFPVACGFNKRVCFAAVGLRLAAAHMARMAVOLMDMSPRIDEDINELIGITF	240							
Dd	181	appnpdawtfpvacgfnnkrvcfaavgrlaaahmarmaavglwmdspridedineligitc	240							
OY	241	I RVTCGEGNLLORANENLVNPVDVDPATATRGRSAASRPTERRPARARSAPRRRV	300							
Dd	241	i rvtcceggnlllgrenelnvpdvqvdaataatigrsaasrpcterpararsarprrv	300							
OY	301 E	301								
Dd	301 e	301								
RESULT	5									
AEO05266										
ID	AEO05266	standard; Protein: 667 AA.								
XX AC	AEO05266;									
XX DT	12-SEP-2001	(first entry)								
XX DE	VP22-Cre fusion protein.									
XX KM	DNA recombinase domain; protein transduction domain; PTD; gene alteration; VP22-Cre fusion protein; Human immunodeficiency virus; HIV; Human spumaretrovirus; HSV,									
XX OS	Chimeric - Human spumaretrovirus.									
XX PD	WO200149832-A2.									
XX PF	12-JUL-2001.									
XX PR	05-JUN--2001; 2001MO-BP00060.									
XX PA	07-JAN-2000; 2000EP-0100351.									
XX PI	10-NOV-2000; 2000EP-0124595.									
XX PT	(ARTE-) ARTEMIS PHARM GMBH.									
XX PS	Schwenk F;									
XX DR	WPI: 2001-441873/47.									
XX N-PSDB;	N-Psdb; AAD09259.									
PT	Using site-specific DNA recombinase domain/protein transduction domain fusion proteins for inducing target gene alterations in organisms or cell cultures -									
CC	Claim 12; Page 35-37; 85pp; English.									
CC	The present invention relates to use of fusion proteins comprising a site-specific DNA recombinase domain e.g. Cre and a protein transduction domain (PTD) e.g. the Human immunodeficiency virus (HIV) derived Tat peptide, for preparing an agent for inducing target gene alterations in a living organism or cell culture. The present invention also provides a method for inducing gene alterations in living organisms using the fusion proteins of the									

CC	Invention. The present sequence is VP22-Cre fusion protein. The
CC	VP22 sequence is from Human spumaretrovirus (HSV).
XX	
SQ	Sequence 667 AA:
	Query Match 100.0%; Score 1561; DB 22; Length 667;
	Best Local Similarity 100.0%; Pred. No. 1,4e-121;
	Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 MTSRSVKSQGPREVPRDEYEDLYTPSSGMASPDSPDTSRRGALQTRSROGEVRFYQY 60
DB	1 mtsrsvksqgprevprdeyedlytpssgmaspsdpdtsrrgalqtsgtqrgevrfyqy 60
OY	61 DESDYALYGSSSEDDHEPVEPTRRPVSGLVSGPGAPARAPPAGSGAGRTTTTAPR 120
DB	61 desdyalygssseddenheveptrrrpvsgavlsgpgparappagsgagrtttlapt 120
OY	121 APTTRRVATTKAAPAAAEETRGKSAOEPSALPPAPASTARTSKTPAOGIARKLHFST 180
DB	121 apttrrvatkapaapaaeltirgksapesaalpdapasctaprsktcpagiarklhstc 180
OY	181 APPNDAPWTPPVAGFENKFECACAVGRLLAMHARMAAYQLMDMSRPRTDEDINELIGITT 240
DB	181 appndapwtpvvaagfknrfecaavgrllaamharmaayqlwmrsrptdedineligtlt 240
OY	241 IRVTVCCEGNILQRANELVNPVDVDAATATRGKSAASRPTERRPARARSARRRPV 300
DB	241 irvtvccegnllqranelvnpdvvdadataatrgksaasrpterpararsarrprvy 300
OY	301 E 301
DB	301 e 301
RESULT 6	
ID	AAE05267 standard; Protein; 747 AA.
XX	AAE05267;
AC	
XX	
DT	12-SEP-2001 (first entry)
XX	
DE	VP22-F1pe fusion protein.
XX	
KM	DNA recombinase domain; protein transduction domain; PTD;
KW	gene alteration; VP22-F1pe fusion protein; Human immunodeficiency virus;
XX	HIV; Human spumaretrovirus; HSV.
OS	Chimeric - Human spumaretrovirus.
OS	Chimeric - Unidentified.
PN	WO200149832-A2.
XX	
PD	12-JUL-2001.
XX	
PF	05-JAN-2001; 2001WO-EP00060.
XX	
PR	07-JAN-2000; 2000EP-0100351.
XX	
PA	10-NOV-2000; 2000EP-0124595.
XX	
PI	(ARTE-) ARTEMIS PHARM GMBH.
XX	
DR	Schwenk F;
XX	
DR	WPI: 2001-441873/47.
XX	
PT	N-PSDB; AAD09260.
XX	
PT	Using site-specific DNA recombinase domain/protein transduction domain
XX	fusion proteins for inducing target gene alterations in organisms or
XX	cell cultures -
PS	Claim 12; Page 40-43; 85pp; English.

XX The present invention relates to use of fusion proteins comprising
 CC a site-specific DNA recombinase domain e.g. Cre and a protein
 CC transduction domain (PTD) e.g. the Human immunodeficiency virus
 CC (HIV) derived TAR peptide, for preparing an agent for inducing
 CC target gene alterations in a living organism or cell culture. The
 CC present invention also provides a method for inducing gene
 CC alterations in living organisms using the fusion proteins of the
 CC invention. The present sequence is VP22-Flpe fusion protein. The
 CC VP22 sequence is from Human spumaretrovirus (HSV).

XX Sequence 747 AA:

Query Match 100.0%; Score 1561; DB 22; Length 747;
 Best Local Similarity 100.0%; Pred. No. 1.6e-121;
 Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSRRSVKSGPREVPDEVEDLYTPSSGMA SPDPSTSRGALOTRSRORGEVRFVQY 60
 DB 1 mtsrrsvksqprevpdevedlytpssgmaspdpstsrqalqtrsrqgevrivgy 60
 QY 61 DESDVALYGGSSSEDDHEPVPTRRPVSGAVLSGFGPARAPPPPAGSGGAGRTPTAPR 120
 DB 61 desdvalyggssseddehpvptrrrpvsqavlsqfgparappppagsggagrtptapr 120
 QY 121 APTQGVATKAPAAPAETTRGRKSAOPESALPDAPASTAPTRSKTPAOGIARKIHFTST 180
 DB 121 aptqgvatkapaapaettrgrksaopsaalpdapastaptrsktptpoglarckihfst 180
 QY 181 APPNDAPWTPPVAGFNKVFCAVGRILAMHARMAAVOLMMSRRTDEDLNELLGITV 240
 DB 181 appndapwtpvpgfnkrfvcaavgrilaamharmavolwmmsrptdedlnellgilt 240
 QY 241 IRTVCEGKNLQIRANELYNPDVQVDATATRGSAASRPTERRAPARSARPRPV 300
 DB 241 irtvcegnllqiranelynpdvqvdaatatrgrsaasrpterraparsarprpv 300
 QY 301 E 301
 DB 301 e 301

RESULT 7

AAE05273
 ID AAE05273 standard; Protein; 683 AA.

XX AAE05273;

DT 12-SEP-2001 (first entry)

DE VP22CreStreptag fusion protein.

XX DNA recombinase domain; protein transduction domain; PTD;
 KW VP22CreStreptag fusion protein; Human immunodeficiency virus; HIV;
 KW gene alteration; Human spumaretrovirus; HSV.

XX ChimERIC - Human spumaretrovirus.

OS ChimERIC - Unidentified.

PN WO200149832-A2.

XX 12-JUL-2001.

PF 05-JAN-2001; 2001WO-EP00060.

PR 07-JAN-2000; 2000EP-0100351.
 PR 10-NOV-2000; 2000EP-0124595.

PA (ARTE-) ARTEMIS PHARM GMBH.

XX Schwenk F;

DR WPI; 2001-441873/47.
 DR N-PSDB; AAD09268.

PT Using site-specific DNA recombinase domain/protein transduction domain
 PT fusion proteins for inducing target gene alterations in organisms or
 PT cell cultures -

PS Disclosure; Page 58-60; 85pp; English.

CC The present invention relates to use of fusion proteins comprising
 CC a site-specific DNA recombinase domain e.g. Cre and a protein
 CC transduction domain (PTD) e.g. the Human immunodeficiency virus
 CC (HIV) derived TAR peptide, for preparing an agent for inducing
 CC target gene alterations in a living organism or cell culture. The
 CC present invention also provides a method for inducing gene
 CC alterations in living organisms using the fusion proteins of the
 CC invention. The present sequence is VP22CreStreptag fusion protein.
 CC The VP22 sequence is from Human spumaretrovirus (HSV).

XX Sequence 683 AA:

Query Match 99.7%; Score 1557; DB 22; Length 683;
 Best Local Similarity 99.7%; Pred. No. 3.2e-121;
 Matches 300; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSRRSVKSGPREVPDEVEDLYTPSSGMA SPDPSTSRGALOTRSRORGEVRFVQY 60
 DB 1 mtsrrsvksqprevpdevedlytpssgmaspdpstsrqalqtrsrqgevrivgy 60
 QY 61 DESDVALYGGSSSEDDHEPVPTRRPVSGAVLSGFGPARAPPPPAGSGGAGRTPTAPR 120
 DB 61 desdvalyggssseddehpvptrrrpvsqavlsqfgparappppagsggagrtptapr 120
 QY 121 APTQGVATKAPAAPAETTRGRKSAOPESALPDAPASTAPTRSKTPAOGIARKIHFTST 180
 DB 121 aptqgvatkapaapaettrgrksaopsaalpdapastaptrsktptpoglarckihfst 180
 QY 181 APPNDAPWTPPVAGFNKVFCAVGRILAMHARMAAVOLMMSRRTDEDLNELLGITV 240
 DB 181 appndapwtpvpgfnkrfvcaavgrilaamharmavolwmmsrptdedlnellgilt 240
 QY 241 IRTVCEGKNLQIRANELYNPDVQVDATATRGSAASRPTERRAPARSARPRPV 300
 DB 241 irtvcegnllqiranelynpdvqvdaatatrgrsaasrpterraparsarprpv 300
 QY 301 E 301
 DB 301 e 301

RESULT 8

AAW95099
 ID AAW95099 standard; Protein; 301 AA.

XX AAW95099;

XX 25-MAY-1999 (first entry)

DE HIV-1 VP22 polypeptide.

XX Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
 KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
 KW Intracellular; transcellular; transcytosis; vascular wound; repair; hair;
 KW smooth muscle; cardiovascular; arteriosclerosis; fibrotic disorder;
 KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
 KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
 KW tachycardia; HIV-1.

OS Human immunodeficiency virus type 1.

PN WO9906540-A2.

PD 11-FEB-1999.
 XX
 XX 29-JUL-1998: 98WO-US151759.
 XX
 XX 29-JUL-1997: 97US-0902572.
 XX
 XX (MITO-) MITOTIX INC.
 XX
 XX Beach DH, Gyuris J, Lamphere L;
 XX
 XX WPI: 1999-153770/13.
 DR N-PSDB: AAX26227.
 PT Fusion and chimaeric proteins including cyclin-dependent kinase
 PT binding motif - used for regulation of cell proliferation and
 PT differentiation, for treatment of, e.g. vascular injury, cancers,
 PT fibrosis and neurodegeneration
 XX
 XX Example 2; Page 26-27; 88pp; English.
 PS
 XX
 CC The invention relates to novel inhibitors of cyclin-dependent kinases
 CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
 CC transfection system (A) that comprises: (i) first gene construct
 CC comprising a sequence encoding an inhibitory polypeptide containing at
 CC least one CDK-binding motif for binding and inhibiting activity of a
 CC CDK, linked to a transcription regulator functional in eukaryotic cells;
 CC (ii) second gene construct comprising a sequence encoding a polypeptide
 CC that promotes endothelialisation, and (iii) a gene delivery composition
 CC for delivering the CGs to a cell for transfection. Also provided are
 CC nucleic acids encoding a fusion protein (FP) containing: (i) a
 CC therapeutic polypeptide sequence (TP) from an intracellular protein that
 CC alters a cellular process when FP enters the cell, and (ii) a
 CC transcellular polypeptide sequence (TCP) that promotes transcytosis of
 CC FP. The FP consists of at least one CDK-binding motif and a TCP. See
 CC AAX26220 for detailed uses of the recombinant transfection system. The
 CC CKI polypeptides are engineered to include any of the peptides shown in
 CC AAW35097-100 encoded by the DNA sequences AAX26225-228.
 XX
 SQ Sequence 301 AA:
 Query Match 99.6%; Score 1554; DB 20; Length 301;
 Best Local Similarity 99.7%; Pred. No. 2e-121;
 Matches 300; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MTSRRSVKSGPRVPRDEYEDLYTPSSGMASSPDPDTSRRGALQTRSRQGEVRFVQY 60
 DB 1 mtsrrsvksgprevpdreyedlytpssgmaspsdpdtsrrgaltqtrsrqgevrivgy 60
 QY 61 DESDYALYGGSSSEDEHPEVPTRRPVSGAVLSGPGPARAPPPAGSGAGRTPTTAPR 120
 DB 61 desdyalygsssedehpevprrtrpvsgavlspgparappppagsgagrtpttapt 120
 QY 121 APRTQVATKAPAPAAETTRGRKSAOPESALPDAPASTAPTRSKTPAGLARKLHFST 180
 DB 121 aptqrvatkapaapaetttrgrksaopesaalpdepastapttrsktpaglarlkhhfst 180
 QY 181 APNPDPAPWTPRVAGFKRFFCAAVGRLAAMHARMAAVQLMDMSRPTDLDLMLGITT 240
 DB 181 appnpdpapwtprvagfkrrffcaavgrlaamharmaaavqlmdmsrptdldlmlgitt 240
 QY 241 IRTVTCGKLLDGRANELVNPVVQDDVDAATATGRSAASRPTEPRPARASASRRPRPV 300
 DB 241 irvtvcgklllqgranelvnpdvvdvdaataatgrsaasrpterparasasrrprpv 300
 QY 301 E 301
 DB 301 e 301
 RESULT 9
 AAY79877
 ID AAY79877 standard; Peptide; 301 AA.

XX AAY79877;
 AC
 XX 10-MAY-2000 (first entry)
 DT
 XX HSV-1 VP22 peptide.
 DE
 XX Papillomavirus; PV; infection; cell proliferation; E2; peptidomimetic;
 KW E1; antiviral; virucide; cytostatic; antiproliferative; dermatological;
 KW preneoplastic lesion; neoplastic lesion; cutaneous lesion; wart;
 KW epidermodysplasia verruciformis; anorectal carcinoma.
 XX
 XX Herpes simplex virus type 1.
 OS
 XX WO200001720-A2.
 PN
 XX 13-JAN-2000.
 PD
 XX 02-JUL-1999: 99WO-US15144.
 PF
 XX 02-JUL-1998: 98US-0091661.
 PR
 XX (HARD) HARVARD COLLEGE.
 PA
 XX Howley P, Benson J, Kasukawa H;
 PI
 XX WPI: 2000-171001/15.
 DR N-PSDB: AAZ88468.
 DR
 XX use of papillomavirus E2 protein peptidomimetics for treating
 PT papillomavirus-infected cells and papillomavirus-induced conditions in
 PT mammals by inhibiting E1-E2 interaction
 PS
 XX Disclosure; Page 42; 110pp; English.
 CC
 CC The present invention describes the use of a small organic compound (A)
 CC which competitively inhibits interaction of a papillomavirus (PV) E2
 CC protein with a PV E1 protein for treating a cell infected with PV or a
 CC mammal with a PV-induced condition. (A) has antiviral, virucide,
 CC cytostatic, antiproliferative and dermatological activities. Methods
 CC from the present invention can be used to treat PV-induced conditions
 CC including growth of PV preneoplastic and neoplastic lesions, cutaneous
 CC lesions chosen from warts and other benign cutaneous lesions, planter
 CC warts (verruca plantaris), common warts (verruca plana), Butcher's
 CC common warts, flat warts, genital warts (condyloma acuminatum) and
 CC epidermodysplasia verruciformis, laryngeal, oral, pharyngeal,
 CC oesophageal and other upper airway papilloma or vaginal, cervical,
 CC vulvar, penile and anorectal carcinoma. The E2 inhibitors may also be
 CC used to treat epithelial and internal fibropapillomas in animals.
 CC The present sequence represents a peptide sequence used in the
 CC exemplification of the present invention.
 CC
 SQ Sequence 301 AA:
 Query Match 99.6%; Score 1554; DB 21; Length 301;
 Best Local Similarity 99.7%; Pred. No. 2e-121;
 Matches 300; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MTSRRSVKSGPRVPRDEYEDLYTPSSGMASSPDPDTSRRGALQTRSRQGEVRFVQY 60
 DB 1 mtsrrsvksgprevpdreyedlytpssgmaspsdpdtsrrgaltqtrsrqgevrivgy 60
 QY 61 DESDYALYGGSSSEDEHPEVPTRRPVSGAVLSGPGPARAPPPAGSGAGRTPTTAPR 120
 DB 61 desdyalygsssedehpevprrtrpvsgavlspgparappppagsgagrtpttapt 120
 QY 121 APRTQVATKAPAPAAETTRGRKSAOPESALPDAPASTAPTRSKTPAGLARKLHFST 180
 DB 121 aptqrvatkapaapaetttrgrksaopesaalpdepastapttrsktpaglarlkhhfst 180
 QY 181 APNPDPAPWTPRVAGFKRFFCAAVGRLAAMHARMAAVQLMDMSRPTDLDLMLGITT 240
 DB 181 appnpdpapwtprvagfkrrffcaavgrlaamharmaaavqlmdmsrptdldlmlgitt 240

Db 181 appndapwtpvafgfnkrvicaavgrlaamharmavqlwmdmsrptdcdlnellgitt 240
 QY 241 IRTVCEGKNLQIRANELVNPVDVDAATATRGSAASRPTERRAPASASRRPRPV 300
 Db 241 IRTVCEGKNLQIRANELVNPVDVDAATATRGSAASRPTERRAPASASRRPRPV 300
 QY 301 E 301
 Db 301 e 301

RESULT 10
 AAB60910
 ID AAB60910 standard; Protein; 301 AA.
 XX AAB60910;
 XX 05-NOV-2001 (first entry)
 DT HSV-1 VP22 protein.
 DE
 XX Co-activator domain; P300/CBP KIX domain; erythrocythaemia; skin disease;
 KW polycythaemia; haemoglobinopathy; cell differentiation; ulcer; cancer;
 KW neurological condition; neurodegenerative disease; immune disease;
 KM diabetes.
 XX Synthetic.
 OS
 XX WO200118036-A2.
 PN 15-MAR-2001.
 PD 31-AUG-2000; 2000WO-US24010.
 PF 03-SEP-1999; 99US-0152402.
 PR (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 PA (JOSL-) JOSLIN DIABETES CENT INC.
 PA Frangioni JV, Cantley LC, Montminy MR;
 XX WPI; 2001-273380/28.
 DR N-PSDB; AAF58996.
 XX
 PT Identifying co-activator domain specific transcriptional activators by
 PT contacting a target domain of a selected transcription factor with a
 PT peptide display library, where the identified binding peptides are
 PT useful for reducing hyperglycemia -
 PS Disclosure; Page 78; 156pp; English.
 XX The present invention describes a method of identifying the co-activator
 XX domain of specific synthetic activators, involving contacting the target
 XX domain of a selected transcription factor with a peptide display library,
 XX and identifying those sequences which bind to the target domain. In
 XX particular, those which bind to the KIX domain of P300/CBP are useful.
 XX The peptides can be used in the treatment of diseases related to aberrant
 XX KIX-dependent gene transcription, including erythrocythaemia,
 XX polycythaemia, haemoglobinopathies, to regulate cell differentiation, to
 XX treat neurological diseases, immunological diseases, diabetes, ulcers,
 XX skin diseases and cancer, and to aid wound healing. The present sequence
 XX is a protein described in the exemplification of the invention.
 SQ Sequence 301 AA;

Query Match 99.6%; Score 1554; DB 22; Length 301;
 Best Local Similarity 99.7%; Pred. NO. 2e-121;
 Matches 300; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTSRSVSGPREVPRDELYTTPSSGMASSPDPSTRGALQTRSRQGEVRFVQY 60
 Db 1 mtsrsvsgprevpredelytppssgmaspsdpstrrgalqtrsrqgevrivqy 60

QY 61 DESDVALYGGSSSEDDHEPVRPRPVSGAVLSGPPARAPPPAGSGAGRTPTTAPR 120
 Db 61 deesdvalyggssseddehpvrprpvsgavlspparapppagsgagrtpttapr 120
 QY 121 APPTORVATKAPAAPAAETTRGRKSAOESALPDAPASTAPTSKTPAQGLAKLHFT 180
 Db 121 apttorvatkapaaettrgrksaopesalpdapastaptsktpaqglaklhft 180
 QY 181 APPNDAPWTPRVAGFNKRVCFAVGRLAAMHARMAAVOLMDMSRPTDDEJNELLGITT 240
 Db 181 appndapwtpvafgfnkrvicaavgrlaamharmavqlwmdmsrptdcdlnellgitt 240
 QY 241 IRTVCEGKNLQIRANELVNPVDVDAATATRGSAASRPTERRAPASASRRPRPV 300
 Db 241 IRTVCEGKNLQIRANELVNPVDVDAATATRGSAASRPTERRAPASASRRPRPV 300
 QY 301 E 301
 Db 301 e 301

RESULT 11
 AAM47194
 ID AAM47194 standard; Protein; 301 AA.
 XX AAM47194;
 XX 03-JUL-1998 (first entry)
 DT
 XX Herpes simplex virus tegument protein VP22.
 DE
 XX HSV; tegument protein; VP22; UL49; antiviral agent; treatment;
 KW cold sore; genital herpes; chickenpox; shingles.
 KM Herpes simplex virus.
 OS
 XX WO9804708-A1.
 PN 05-FEB-1998.
 PD 28-JUL-1997; 97WO-GB02036.
 PF 26-JUL-1996; 96GB-0015726.
 PR (MEDI-) MEDICAL RES COUNCIL.
 PA Hope RG, McGeoch DJ, McLaughlan J, Rixon HM;
 XX WPI; 1998-130696/12.
 DR N-PSDB; AAV17085.
 XX
 PT New antiviral agent disrupting binding of VP22 to VP16 or gB -
 PT useful for treating infections caused by herpes simplex, e.g. cold
 PT sores and chicken-pox
 PS Example; Pages 49-50; 75pp; English.
 XX The present sequence is the herpes simplex virus (HSV)
 XX tegument protein VP22. VP22 was used in the preparation of a novel
 XX antiviral agent, which inhibits the maturation and/or replication
 XX of HSV by disrupting association between VP22 and VP16 and/or gB.
 XX The agent can be used to treat, e.g. cold sores, genital herpes,
 XX chickenpox and shingles.
 SQ Sequence 301 AA;

Query Match 99.5%; Score 1553; DB 19; Length 301;
 Best Local Similarity 99.7%; Pred. NO. 2.5e-121;
 Matches 300; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTSRSVSGPREVPRDELYTTPSSGMASSPDPSTRGALQTRSRQGEVRFVQY 60
 Db 1 mtsrsvsgprevpredelytppssgmaspsdpstrrgalqtrsrqgevrivqy 60

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Db      1 mstrsvksqpreyrdedyedlylpsqsgmaspdpstlrsgalqtrsgvgrfvy 60
Qy      61 DESDYLGGSSSEDEHPEVPRTRRPVSGAVLSGPGPARAPPAGSGAGRTPTTAPR 120
Db      61 desdyalygssseddehpvprtrirpvsavlsqpgparpppagsgagrtptapr 120
Qy      121 APRQVATRKAPAAPAAETTRGRKSAQEPESALPDAPASTAPTRSKTPAQGLARKLHFS 180
Db      121 aprtrvatckapaaaeetrgrksaqpesaalpdapastaptrsktpaqglarklhfs 180
Qy      181 APPNDAPWTPRVAGFNKRVFCAVGLAAMHARMAAQLMDMSRPRTDEDLNLGLITTT 240
Db      181 appndapwtprvagfnkrfvcaavgrlaamharmavqlmdmsrprtdedlnellgltc 240
Qy      241 IRTVVEGKNLLQRLNELVNPVDVDAATATGRSAASRPTRPRAPARSARRRPV 300
Db      241 lrtvceegknllqranelvnpdvvdadatatgrsaastrprtrpapsarrprpv 300
Qy      301 E 301
Db      301 e 301

```

RESULT 12

AA983261 ID AAY83261 standard; Protein: 301 AA.

XX AAY83261:

DT 16-AUG-2000 (first entry)

DE HSV-1 V22 cellular localisation signal sequence.

KW Ubiquitin ligase; SCF; F-box protein; targeted degradation;

KM destabilisation; proteolysis; drug discovery; gene therapy; cancer;

XX oncoprotein; Huntington's disease; gene knockout; delivery systems.

OS Synthetic.

XX Herpes simplex virus-1.

XX WO200022110-A2.

XX 20-APR-2000.

XX 08-OCT-1999; 99WO-US23705.

XX 09-OCT-1998; 98US-0103787.

XX (HARD) HARVARD COLLEGE.

XX Zhou P, Howley P;

XX WPI: 2000-317970/27.

XX N-PSDB: AA293717.

XX Targeting degradation of polypeptide useful for treating cancer and

XX other proliferative disorders, involves conjugating polypeptide with

XX ubiquitin protein ligase or inhibiting ubiquitination using organic

XX compound

XX Disclosure: Page 76; 185pp; English.

XX The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin

XX ligases) which can be used for the targeted degradation of a target

XX polypeptide in vivo. Targeted degradation is achieved by expressing

XX the ubiquitin ligase in a cell linked to the interaction domain of

XX the target polypeptide and thereby recruiting the target polypeptide

XX to the ubiquitin ligase. Such methods are useful for decreasing or

XX increasing the level of a target polypeptide and for creating and

XX expressing a destabilized polypeptide which is subjected to SCF

XX mediated proteolysis. Degrading any desired protein in a cell is

XX useful for preventing or treating diseases caused by the presence of

CC abnormal amount of the specific polypeptides, for drug discovery and
 CC for gene therapy. Diseases treated include cancer, by degradation of
 CC oncoproteins, Huntington's disease, other proliferative disorders and
 CC microbial infections. The method provides a quick and easy
 CC alternative to gene knockout technology. The target polypeptide can
 CC be degraded at all stages, or a specific stage, of development in the
 CC mature animal. The hybrid ubiquitin ligase may also include an
 CC optional localisation sequence such as this HSV-1 V22 sequence.

Sequence 301 AA;

Query Match

Best Local Similarity 99.7%; Score 1553; DB 21; Length 301;

Matches 300; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy      1 MTSRSVKSQPREYRDYEDLYTPSSGMA SPDPSTSRGALQTRSGRGEVRYQY 60
Db      1 mstrsvksqpreyrdedyedlylpsqsgmaspdpstlrsgalqtrsgvgrfvy 60
Qy      61 DESDYLGGSSSEDEHPEVPRTRRPVSGAVLSGPGPARAPPAGSGAGRTPTTAPR 120
Db      61 desdyalygssseddehpvprtrirpvsavlsqpgparpppagsgagrtptapr 120
Qy      121 APRQVATRKAPAAPAAETTRGRKSAQEPESALPDAPASTAPTRSKTPAQGLARKLHFS 180
Db      121 aprtrvatckapaaaeetrgrksaqpesaalpdapastaptrsktpaqglarklhfs 180
Qy      181 APPNDAPWTPRVAGFNKRVFCAVGLAAMHARMAAQLMDMSRPRTDEDLNLGLITTT 240
Db      181 appndapwtprvagfnkrfvcaavgrlaamharmavqlmdmsrprtdedlnellgltc 240
Qy      241 IRTVVEGKNLLQRLNELVNPVDVDAATATGRSAASRPTRPRAPARSARRRPV 300
Db      241 lrtvceegknllqranelvnpdvvdadatatgrsaastrprtrpapsarrprpv 300
Qy      301 E 301
Db      301 e 301

```

RESULT 13

AA96574 ID AAY96574 standard; Protein: 297 AA.

XX AAY96574:

DT 12-SEP-2000 (first entry)

DE HSV-1 VP22 polypeptide.

KW hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;

KM retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;

KW INK4; HSV-1; VP22; fusion protein.

OS Herpes simplex virus 1.

XX WO200031238-A2.

XX 02-JUN-2000.

XX 24-NOV-1999; 99WO-US27907.

XX 25-NOV-1998; 98US-0109891.

XX 17-FEB-1999; 99US-0120549.

XX (GENE-) GENETICA INC.

XX Hannon GJ, Beach DH;

XX WPI: 2000-400055/34.

XX N-PSDB: AAA29395.

XX New method for increasing the proliferative capacity of cell lines
PT comprises administering agents reversibly activating telomerase
PT activity and reversibly inactivating Rb/INK4 and/or p53 pathways useful
PT in treating age related diseases

PS Disclosure: Page 31-32; 123pp; English.

XX The HSV-1 VP22 polypeptide can be fused to a retinoblastoma (Rb)
XX inactivator protein sequence to aid targeting and internalization.
CC The invention concerns methods and reagents for extending the life-span,
CC e.g. the number of mitotic divisions, of a cell. The method relies on
CC activation of a telomerase activity and inhibition of one or both of a
CC Rb/INK4 pathway or a p53 pathway. Phosphorylation of Rb by
CC cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the
CC division cycle. Binding of INK4 family members, e.g. the tumour
CC suppressor p16INK4a, inhibits kinase activity and results in growth
CC arrest. Rb inactivators can selectively and reversibly inactivate an
CC Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MDM2
CC is a cellular inhibitor of Rb/E2F function and the p53 tumour suppressor
CC and can also be used in the methods. Other molecules which can be used
CC include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which
CC differs from at one or more of residues K22, R24, H95 and/or D97.
CC Additional constructs include a papilloma virus E7 protein, or other
CC viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of
CC the Rb and p16INK4a genes may also be used. The methods are useful for
CC increasing the proliferative capacity of cells. The cells are
CC subsequently of use in pharmaceutical and cosmetic preparations used to
CC treat conditions related to (premature) ageing, e.g. macular degeneration
CC and arteriosclerosis. The cells can also be used to replace tumour cell
CC lines in vitro and for studies on biochemical and physiological aspects
CC of growth and differentiation. Long lived (immortal) cells could also be
CC of use in the production of normal or genetically engineered
CC biotechnology products.

XX Sequence 297 AA:

Query Match 97.4%; Score 1520; DB 21; Length 297;
Best Local Similarity 98.3%; Pred. No. 1.4e-118;
Matches 296; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

QY 1 MTSRSVSGPREVREDEEDLYTPSSGMA SPDSPPTSRGALQTRSGGEVRFYQY 60
DB 1 mtsrsvsgprevr-----dlytpssgmaspdspptsrgralqtrsggrvrfyqy 56
QY 61 DESDYALYGSSSEDEHPEVPRTRRPVSGAVLSGPPARAPPPAGSGAGRTPTTAPR 120
DB 57 desdyalygsssedehpevprtrrpvsgavlsppparappppagsgagrtpttpr 116
QY 121 APRQGVATKAPAAPAETTRGRKSAOPESALPDAPASTATRSKTPAOGIARKLHST 180
DB 117 aprtqvatkapaapaettrgrksaopesaalpdpastatrtsktpagiarlrlhst 176
QY 181 APNPDAWTPPVAGFNKRVFCAAGRLAAMHARMAAVALMDMSRPDDEDNELIGITTT 240
DB 177 appnpdwpkvprvagfnkrfvcaagrglaamharmaaavqlwmsprcdedinelilgtt 236
QY 241 IRTVYCEGKNLIQRANELVNDVODVDAATATRGSAASRPTERRPARPARSASRRPRV 300
DB 237 lrtvcegknllqratelvpndvqvdaataatrgsaasrpterrparparsasrrprpv 296
QY 301 E 301
DB 297 e 297

RESULT 14
AAB86330
ID AAB86330 standard; Protein: 267 AA.
XX AAB86330;
AC
XX

DT 18-SEP-2001 (first entry)
DE VP22 protein fragment VP22deltaC.
XX
XX Fusion protein: VP22; E7; cell import signal; cell export signal;
KW antigen; immunization; infection-induced auto-immune disease;
KW tumor disease.

XX Unidentified.

XX WO200151516-A2.

XX 19-JUL-2001.

XX 15-JAN-2001; 2001WO-DE00134.

XX 13-JAN-2000; 2000DE-1001230.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Mueller M, Michel N, Osen W, Gissmann L, Zentgraf H;

XX WPI: 2001-442135/47.

PT Identifying an immunization agent comprising cell import and/or
PT export signal sequences and an antigen for immunizing against
PT infection-induced auto-immune and tumor disease

PS Disclosure: Fig 4; 23pp; German.

CC This invention describes a fusion protein comprising cell import and/or
CC export signal sequences and an antigen which is suitable for immunizing
CC an individual against a disease, together with a DNA that codes for said
CC protein. The invention also relates to the use of the protein (II) and
CC its encoding DNA (I) for immunizing an individual against diseases. In
CC particular against infection-induced auto-immune and tumor disease. This
CC sequence represents the VP22 protein fragment VP22deltaC used in the
CC construction of the fusion constructs described in the method of the
CC invention.

XX Sequence 267 AA:

Query Match 89.2%; Score 1392; DB 22; Length 267;
Best Local Similarity 100.0%; Pred. No. 5.4e-108;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSRSVSGPREVREDEEDLYTPSSGMA SPDSPPTSRGALQTRSGGEVRFYQY 60
DB 1 mtsrsvsgprevr-----dlytpssgmaspdspptsrgralqtrsggrvrfyqy 60
QY 61 DESDYALYGSSSEDEHPEVPRTRRPVSGAVLSGPPARAPPPAGSGAGRTPTTAPR 120
DB 61 desdyalygsssedehpevprtrrpvsgavlsppparappppagsgagrtpttpr 120
QY 121 APRQGVATKAPAAPAETTRGRKSAOPESALPDAPASTATRSKTPAOGIARKLHST 180
DB 117 aprtqvatkapaapaettrgrksaopesaalpdpastatrtsktpagiarlrlhst 180
QY 181 APNPDAWTPPVAGFNKRVFCAAGRLAAMHARMAAVALMDMSRPDDEDNELIGITTT 240
DB 177 appnpdwpkvprvagfnkrfvcaagrglaamharmaaavqlwmsprcdedinelilgtt 240
QY 241 IRTVYCEGKNLIQRANELVNDVODV 267
DB 241 lrtvcegknllqratelvpndvqvdaataatrgsaasrpterrparparsasrrprpv 267

RESULT 15
AAV78333
ID AAV78333 standard; peptide: 246 AA.
XX AAV78333;
AC

XX 04-MAY-2000 (first entry)

DE Herpes simplex virus VP22 protein SEQ ID NO:5.

KW Cell membrane permeant; medical imaging; diagnosis; radiotherapy;
pharmaceutical therapy; drug delivery.

XX Herpes simplex virus.

XX WO967284-A2.

XX 29-DEC-1999.

XX 18-JUN-1999; 99WO-US13660.

XX 20-JUN-1998; 98US-0090087.

XX (UNITW) UNIV WASHINGTON.

XX Plvnicia-Worms D;

XX WPI: 2000-160576/14.

XX New membrane permeant peptide complexes for medical imaging,
diagnostics and therapy

PS Claim 3; Page 17; 65pp; English.

CC The present invention describes compound comprising a cell membrane
permeant peptide, a diagnostic or an active substance and a functional
linker moiety linking them, where the functional linker moiety confers
target cell specificity to the compound or a salt of the compound. The
compounds and compositions are useful in the fields of medical imaging,
diagnostics and pharmaceutical therapy. The composition are for medical
imaging, evaluating intracellular processes, radiotherapy of
intracellular targets and drug delivery. The cell membrane permeant
peptides conjugate coordination and covalent complexes have target cell
specificity, therefore, the Tat peptide and other cell membrane permeant
peptides can be used to selectively deliver non- or poorly permeant
drugs, diagnostic substances such as oligonucleotides, peptides, peptide
nucleic acids, fluorochromes, dyes, enzyme substrates and metals useful
in medical therapy, imaging and/or diagnostics selectively to cells
in vivo only when functional linkers are introduced into permeant peptide
constructs. The present sequence represents a specifically claimed
cell membrane permeant peptide from the present invention.

SO Sequence 246 AA:

Query Match 77.1%; Score 1203.5; DB 21; Length 246;
Best Local Similarity 80.7%; Pred. No. 2,4e-92;
Matches 243; Conservative 0; Mismatches 3; Indels 55; Gaps 2;

QY 1 MTSRSKVGSGPRVPRDEDELYTTPSSGMSFSDSPDTSRKALOTRSRQGEVRFVQY 60
|||||
DB 1 MTSRSVKSQPREVPRDEDELYTTPSSGMSFSDSPDTSRKALOTRSRQGEVRFVQY 60
|||||
QY 61 DESDVALYCGSSSEDEHPEVPRTRRRVSGAVLSCGPPARAPPPAGSGAGRTPTAPR 120
|||||
DB 61 desdvaly99ssedehpevprtrrrvsgavls99pparapppags99agrtptapt 120
|||||
QY 121 APPTORVATKAPAPAAETTRGRKSAQPSAALPDAPASTAPTRSKTPAQGLARKLHFST 180
|||||
DB 121 apttgrvatkapaapaettrgrksaqpsaalpdapastapt----- 163
|||||
QY 181 APPNPAPMPTRVAGFNKRVFCAVGRLLAAMARMAVOLMDKSRPTDEDLNELIGITT 240
|||||
DB 164 -----vqlwmsrptdedlnellgltth 186
|||||
QY 241 IRVTGCEGNLORANELVNPVVDVDAATATRGSAASRPTERRARAPARSASRRRPV 300
|||||
DB 187 -rvtvcegnllqranelvnpdvvgvdaatatrgrsaasrpterraraparsasrrprpv 245

Qy 301 E 301
|
Db 246 e 246

Search completed: August 28, 2002, 12:23:40
Job time: 324 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 12:20:31 ; Search time 17.53 Seconds
(without alignments)
1649.908 Million cell updates/sec

Title: US-09-522-278b-12

Sequence: 1 MTSRRSVKSGPREVPDEYE.....PTERRPAPARSASRRPRPV 301

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1561	100.0	301	1 WMBEP9	UL49 protein - hum
2	303	19.4	304	1 WZBEA9	33.2K tegument pro
3	270.5	17.3	290	1 S36706	B4 protein - equin
4	270.5	17.3	304	2 T42554	tegument protein -
5	245.5	15.7	195	2 S24228	BHY-1 protein homo
6	225.5	14.4	302	1 WZBE9	gene 9 protein - h
7	211	13.5	249	2 S60741	major tegument pro
8	210	13.5	249	2 UQ2201	UL49 protein - Ma
9	161.5	10.3	660	1 QOBE3	BHFL1 protein - hu
10	161	10.3	1460	1 EDBE1F	immediate-early pr
11	153.5	9.8	1446	1 A45344	glycoprotein A - m
12	149	9.5	846	2 S52418	hypothetical prote
13	146.5	9.4	395	2 H75457	hypothetical prote
14	146	9.4	839	2 F75518	hypothetical prote
15	144	9.2	1037	2 B87254	translational initia
16	144	9.2	1201	2 G86441	unknown protein (i
17	140.5	9.0	1282	2 JE0120	glycoprotein A - m
18	140.5	9.0	1952	2 T48814	hypothetical prote
19	140	9.0	1132	2 C75259	probable iron-sulf
20	139.5	8.9	932	2 T21338	hypothetical prote
21	139	8.9	438	1 WMBE38	arylesterase-relat
22	138	8.8	358	1 WMBE38	infected cell prot
23	137	8.8	590	1 T35297	probable dihydrol
24	137	8.8	1069	2 S27922	nuclear antigen EB
25	136.5	8.7	1320	2 JC5630	TCOF1 protein - mo
26	135.5	8.7	754	2 B97586	hypothetical prote
27	135.5	8.7	754	2 AC2807	Ompa family protei
28	135	8.6	261	1 WMBEXE	infected cell prot
29	134.5	8.6	3149	1 QOBE8	BPFL1 protein - hu

30	134	8.6	2187	2 T30826	nascent polypeptid
31	130	8.3	507	2 T44768	antifreeze glycope
32	130	8.3	858	2 S15762	neurofilament trip
33	129.5	8.3	550	2 C75557	hypothetical prote
34	129.5	8.3	901	2 A49227	sialidase - Actino
35	129	8.3	375	2 T08134	oleosin-like prote
36	129	8.3	509	2 T34871	probable membrane
37	128	8.2	725	2 T33498	hypothetical prote
38	128	8.2	2022	2 T48818	glucan 1,4-alpha-g
39	127.5	8.2	608	2 A35021	myosin-light-chain
40	127.5	8.2	822	2 T51049	related to nucleol
41	127	8.1	1791	2 T02345	hypothetical prote
42	127	8.1	3164	1 WMBEH6	ul36 protein - hum
43	126.5	8.1	476	2 T27051	hypothetical prote
44	126.5	8.1	628	2 J00110	hypothetical 69k p
45	126.5	8.1	801	2 T29018	hypothetical prote

ALIGNMENTS

RESULT 1	
WMBEP9	
UL49 protein - human herpesvirus 1 (strain 17)	
C:Species: human herpesvirus 1	
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jun-2000	
C:Accession: D30089	
R:McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; P	
J. Gen. Virol. 69, 1531-1574, 1988	
A:Title: The complete DNA sequence of the long unique region in the genome of herpes	
A:Reference number: A30083; MUID:88274327	
A:Accession: D30089	
A>Status: nucleic acid sequence not shown; translation not shown	
A:Molecule type: DNA	
A:Residues: 1-301 <MCG>	
A:Cross-references: GB:X14112; NID:g1944536; PIDN:CAA32299.1; PID:g59549; GB:D00317	
A:Genetics:	
A:Gene: UL49	
C:Superfamily: varicella-zoster virus gene 9 protein	
Query Match	100.0%; Score 1561; DB 1; Length 301;
Best Local Similarity	100.0%; Pred. No. 6.4e-86;
Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 MTSRRSVKSGPREVPDEYEDLYTPSSGMA SPDSPPDTSRRGALQTRS RQGEVRFVQY 60	
DB 1 MTSRRSVKSGPREVPDEYEDLYTPSSGMA SPDSPPDTSRRGALQTRS RQGEVRFVQY 60	
QY 61 DESDVALGSGSSDEDEHPEVRRTRRPVSGAVLSGPGARAPPPAGSGGACRTPTTAPR 120	
DB 61 DESDVALGSGSSDEDEHPEVRRTRRPVSGAVLSGPGARAPPPAGSGGACRTPTTAPR 120	
QY 121 APTROVATKAPAAPAETTRGRKSAOPESALPPAPASTATPRTSKTPAGGLARKLHFTST 180	
DB 121 APTROVATKAPAAPAETTRGRKSAOPESALPPAPASTATPRTSKTPAGGLARKLHFTST 180	
QY 181 APTNDAPPTPVAGFENKRVFCAAVGRLAAMHARMAAVALMDMSRPRTDEDLNLGITT 240	
DB 181 APTNDAPPTPVAGFENKRVFCAAVGRLAAMHARMAAVALMDMSRPRTDEDLNLGITT 240	
QY 241 ITVTVCCEGKNLLORANELVNPVVDVDAATATTRGRSAASRTTERPRAPARSASRRPRV 300	
DB 241 ITVTVCCEGKNLLORANELVNPVVDVDAATATTRGRSAASRTTERPRAPARSASRRPRV 300	
QY 301 E 301	
DB 301 E 301	
RESULT 2	
WZBEA9	
33.2K tegument protein - equine herpesvirus 1 (strain Ab4p)	

C:Species: equine herpesvirus 1
A:Note: host Equus caballus (domestic horse)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 16-Jul-1999
C:Accession: C36796
R:TelFord, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
submitted to GenBank, March 1992
A:Description: The DNA sequence of equine herpesvirus-1.
A:Reference number: A36805
A:Accession number: C36796
A:Molecule type: DNA
A:Residues: 1-304 <TEL>
A:Cross-references: GB:M86664; NID:g330791; PIDN:AA802446.1; PID:g330803
R:TelFord, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
Virology 189, 304-316, 1992
A:Title: The DNA sequence of equine herpesvirus-1.
A:Reference number: A41831; NUID:92295566
A:Contents: annotation; possible protein-coding frames
A:Note: neither amino acid nor nucleotide sequence is given
C:Genetics:
A:Gene: 11
C:Superfamily: varicella-zoster virus gene 9 protein

```

Query Match Similarity      19.4%; Score 303; DB 1; Length 304;
Match Local Similarity     32.4%; Pred. No. 2.6e-11;
Matches    93; Conservative   30; Mismatches    96; Indels    68; Gaps    11;

Qy      21 DLYVPPSSGMA SPDSPPTRSRGALQTSRNGCEFRFYQ-----YDESDDALYGSGSSS 73
          ||| : ||| : ||| : | : | : | : | : | : | : | : | : | : | : | : |
Db      58 DLYES-----ASPNDKYKTRRG -MSTAHHYHSDSEHYETCGDEFDYDACEVSLIG--- 108
          ||| : ||| : ||| : | : | : | : | : | : | : | : | : | : | : | : |

Qy      74 EDDEHEVPRTRRPVSGAVLSGPG--PARAPPPAGSGGAGRTPPTTAPRAERTGRVATK 130
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      109 -----GKLSTNGSQSPAKAQPPRGGAAA--PPRVAYTRPPTAAAT- 149
          ||| : ||| : ||| : | : | : | : | : | : | : | : | : | : | : | : |

Qy      131 APAAPAEETRRKRKSAGPESALPLPAAPASTARTSKTTPAOGIARLKHSTAPPNDAPT 190
          ||| : ||| : ||| : | : | : | : | : | : | : | : | : | : | : | : |
Db      150 -----STTPROODCAPKQRASPG-----VNRIKSGKGIA----FSGTRPKPSOMY 191
          ||| : ||| : ||| : | : | : | : | : | : | : | : | : | : | : | : |

Qy      191 PRVAFGNKRVCAAGRLAHAMAAVAOLMMSPRTEDEDINELGITITVTVCCEGN 250
          ||| ||||| ||| ||| ||| ||| : ||| : ||| : ||| : ||| : |||
Db      192 CATHLFNKKVFCAAASRNAHAHASDAASLPWLNPPKLTIEDLDREIKAAAIRILVCEGAQ 251
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy      251 LLOARNELVNPDPVDVDAATATGRGSASRPTEPRPARARSASPR 297
          ||| : ||| : ||| : | : | : | : | : | : | : | : | : | : | : | : |
Db      252 LLEVANSTME-----STPGGYAACGNGIDRRP-RTASRRR 286
          ||| : ||| : ||| : | : | : | : | : | : | : | : | : | : | : | : |

RESULT      3
S36706
B4 protein - equine herpesvirus 4
C:Species: equine herpesvirus 4
C:Date: 09-Jun-1994 #sequence_revision 12-May-1995 #text_change 20-Jun-2000
C:Accession: S36706
R:Rigilo, P.
submitted to the EMBL Data Library, November 1989
A:Reference number: S36703
A:Accession: S36706
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-290 <Ric>
C:Superfamily: varicella-zoster virus gene 9 protein

```

```
Query Match Similarity      17.3% Score 270.5 DB 2 Length 290;
Best Local Similarity       34.4% Pred No. 2.1e-09;
Matches      85; Conservative 18; Mismatches 77; Indels 67; Gaps 11;
```

Oy 60 YDESVDYALGCGSSSEDDHEVPRTTRRPVSGAVLSGPC---PARAPPAGSCGAGRPT 116
|||:|:| | | : | : | : | : | : |||
Db 84 YDACEYSILVG-----GLRISHGRSLPRTKTPHAK---SAGVIP- 120

```

QY 117 TAPRNPRTQVATKAPARAPAAETTRGKRSKAPQESALRDPDAPASPTPRSTPAQGL--AA 174
Db 121 -----PQRV-----PAPRAT-----RAAP--SATPTPQDCAVAKORTSPGVNSTIKSGK 161
QY 175 KLHESTARPNDAEMTPTRVAGFNKRVFCAAVGRLAAMHARMAAVOLVMDMSRPTDEDLNE 234
Db 162 SLARSCPTKPKPTKTMUGATHTLFKNKVFCAAVSRVMAAANSDAASALDLDPRPTNEDLDR 221
QY 235 LIGITTTIRVTVCEGKNLLQRRANELVNPDRVQDDAATATATGRS-----AASRPTEPRRPARA 290
Db 222 FLKAAATIRILVCEGSKLEEMAN-----ATMERSPDGAAGAAVAPRGYDRRP-- 265
QY 291 RSASRPR 297
Db 266 RLASRRR 272

```

```

RESULT      4
T42554
Legend: protein = equine herpesvirus 4 (strain NS80567)
C:Species: equine herpesvirus 4
A:Variety: strain NS80567
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C:Accession: T42554
R:RefId: E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.
J. Gen. Virol. 79, 1197-1203, 1998
A:Title: The DNA sequence of equine herpesvirus-4.
A:Reference number: 222173; MUID:98264497
A:Accession: T42554
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-304 <TEL>
A:Cross-references: EMBL:AF030027; NID:g2605950; PIDN:AAC59525.1; PID:g2605953
C:Experimental source: strain NS80567
C:Genetics:
A:Gene: 11
C:Superfamily: varicella-zoster virus gene 9 protein

```

Query Match	17.3%	Score 270.5	DB 2	Length 304	
Best Local Similarity	34.4%	Pred. 2.2e-09			
Matches 85	Conservative 18	Mismatches 77	Indels 67	Gaps 11	
Qy	60	YDESQYALYGGSSSEDDHEVPRTRRPVSGAVLSGPG---PARAPPAGSGAGRTPT	116		
		: :		: :	
Db	98	YDACEYSLVGG-----GLTSHSGHGLSTPTKTTPHK---SAGYTP	134		
Qy	117	TAPRAPRTQRYATKAPAPAAETTRGKRKSAPQESALPDAPASTAPTRSKTPAQGL--AR	174		
		: :		: :	
Db	135	-----PQRV---PARPAT-----RAAP--SATPTQPCVAKORTSPGVNSIKSGK	175		
Qy	175	KIHSTAPPNDPAWPTPRVAGFNKRYFCACAVGRLLAAMHARMAAVOLWMDSRPTDEDLNE	234		
		: :		: :	
Db	176	SLAFSECTKPTKPTPYGATHTLFNKHVFCAAVSRVAAAHNSDAASALWLMDIDPRTKTEDLDR	235		
Qy	235	LLGITITIVTVEGKNLLQRANELYNPDVQVVDATAATARGS----AASRTERPRAPA	290		
		: :		: :	
Db	236	FLKAAAIRILVCEGSKLLEMAN-----ATMERSPDGAAVAADIGYDRP-	279		
Qy	291	RSASRRP 297			
		: :		: :	
Db	280	RLASRRR 286			

RESULT 5
S24228
BHV-1 protein homolog VZV9 - bovine herpesvirus 1 (fragment)
C.Species: bovine herpesvirus 1
C.Date: 09-Jun-1994 #sequence_revision 29-Aug-1997 #text_change 03-Nov-2000
C.Accession: S24228
R.Misra, V.
submitted to the EMBL Data Library, January 1992
A.Reference number: S24228

A:Accession: S24228
A:Molecule type: DNA
A:Residues: 1-195 <MIS>
A:Cross-references: EMBL:Z11610
C:Superfamily: varicella-zoster virus gene 9 protein

Query Match 15.7%; Score 245.5; DB 2; Length 195;
Best Local Similarity 32.1%; Pred. No. 4.4e-08;
Matches 62; Conservative 24; Mismatches 98; Indels 9; Gaps 3;

OY 99 ARAPPAGSGAGRTPTTAPRAPRTQVATKAPAA-----AETTRGRKSAQPSAAL 153
DB 7 ARGRDRAAAAGTTVAAPAAPARSSSRPPRAADPPVLRPATRGSSGAGAVAVG 66
OY 154 PDAPASTARTSKTPAQGLARKHSTAPNPDPAPPTPVAGNKKVFCFAVRLAAMA 213
DB 67 P--PRAPPGANAVASG--RPLAFSAAPKTPKAPWCPTHAANRTIFCEAVLVAAEYA 122
OY 214 RMAAVQMDMSRPRTDEDINELLGITITRVTCCEKNLORANELVNPVODVDAATAT 273
DB 123 RQAASVWSDPPKSNERRDRMLKSAIRLVCEGSLAANDIILAAARQAPANGSTS 182
OY 274 RGRSAASRPTERP 286
DB 183 GGESRLRGERARP 195

RESULT 6
W2BE9
gene 9 protein - human herpesvirus 3
C:Species: human herpesvirus 3, varicella-zoster virus
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999
C:Accession: J27212
R:Davidson, A.J.; Scott, J.E.
J. Gen. Virol. 67, 1759-1816, 1986
A:Title: The complete DNA sequence of varicella-zoster virus.
A:Reference number: A27345; MUID:8630657
A:Accession: J27212
A:Molecule type: DNA
A:Residues: 1-302 <DAV>
A:Cross-references: EMBL:X04370; MID:g59989; PIDN:CAA27892.1; PID:g59998
C:Genetics:
A:Gene: 9
C:Superfamily: varicella-zoster virus gene 9 protein

Query Match 14.4%; Score 225.5; DB 1; Length 302;
Best Local Similarity 26.2%; Pred. No. 1e-06;
Matches 89; Conservative 27; Mismatches 107; Indels 117; Gaps 10;

OY 2 TSTRSKVSGP-----REVPDEYEDLYTPSSGMSAPSPDPTSRGALQ 46
DB 29 TARSRVVGPPDDSDSLGYTTVGADSPSPVADLYFEHKNTTPRHQPNDS----- 82
OY 47 TTSRQNGEVRFQYDESDYALYGGSSSEDEDEHEVPRTRR-----VSGAVLSGPGR 99
DB 83 -----GSEDDDEDIDEVVAARREARLRHELVEDAVENPLSY 119
OY 100 RAPPPAGSGAGRTPTTAPRAPRTQVATKAPAPAAETTRGRKSAQPSAALPDAPAS 159
DB 120 EKP-----SRPFTKNA-----VKRK-----LEDSP-K 141
OY 160 TAPTRSKTPAQGLARKHSTAPNPDPAPPTPVAGNKKVFCFAVRLAAMAHAAYO 219
DB 142 RAPPGAGTASG--RPISSTAPKTATSSWCGPTPSYKRVFCEAVRVAAMAQAKAARA 199
OY 220 LMDMSRPRTDEDINELLGITITRVTCCEKNLORANE----- 257
DB 200 ANNSNPFRNNAELDRLLTGAIVRTIYHEGLINLQANNEADLGEASVSRGHNKRTGDIQ 259
OY 258 --LVNPDVVDVDAATATRGSAASRPTERPAPASASR 295

DB 260 GGMGNPEMYAQYRKPKSRDTDTQTGRITNRSR--ARSASR 297

RESULT 7

major tegument protein VP22 homolog - Marek's disease virus
C:Species: Marek's disease virus
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S60741

R:Kopidesova, D.; Kopacek, J.; Zelnik, V.; Ross, N.L.J.; Pastorekova, S.; Pastorek, Arch. Virol. 140, 355-362, 1995
A:Title: Identification and characterization of a cDNA clone derived from the Marek's A:Reference number: S60741; MUID:95325753
A:Accession: S60741

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-249 <KOP>
A:Cross-references: EMBL:X73370

Query Match 13.5%; Score 211; DB 2; Length 249;
Best Local Similarity 25.9%; Pred. No. 6.2e-06;
Matches 74; Conservative 33; Mismatches 93; Indels 86; Gaps 9;

OY 38 DTSRRCALGTRSRQGEVRFQYDESDYALYGGSSSEDEDEHEVP-----RTRRPVSGA 91
DB 3 DSERRKSSERRS-----LGTPSAVD--VSIAPRRSTKQRLNOD 42
OY 92 VLSGPPARAPPPAGSGAGRTPTTAPRAPRTQV-ATKAPAPAAETTRGRKSAOPES 150
DB 43 DLSKHGPFTHDP-----TQKYKSAKAVSEDSVSTTRGGFTNKP-- 80
OY 151 AALPDAPASTAPTRSKTPAQGL-ARKLHSTAPNPDPAPPTPVAGNKKVFCFAVRLA 209
DB 81 -----RAKPGVAAVQSNKFAFSTAPSASSTWRNMTVAENMFCGAAVATVA 127
OY 210 AMHARMAAVQMDMSRPRTDEDINELLGITITRVTCCEKNL-----LQ 253
DB 128 QYHAYOGALALMRQDPPRTNEELDAFLSRAVYITTIQEGPNLGEAETCARLLSEGLS 187
OY 254 RANELVNPVODVDAATATRG-----RSAASRPTERPAPAS 292
DB 188 QGNENVRKSKSERTTSETRRGCEIEIKSPDPSHRTHNRPATYS 233

RESULT 8

JQ2201
UL49h protein - Marek's disease virus
C:Species: Marek's disease virus
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Oct-1999
C:Accession: JQ2201
R:Yanagida, N.; Yoshida, S.; Nazertan, K.; Lee, L.F.
J. Gen. Virol. 74, 1837-1845, 1993
A:Title: Nucleotide and predicted amino acid sequences of Marek's disease virus homol A:Reference number: JQ2199; MUID:93389438
A:Accession: JQ2201

A:Molecule type: DNA
A:Residues: 1-249 <YAN>
A:Cross-references: GB:L10283; MID:g388703; PIDN:AAA03148.1; PID:g388706
A:Experimental source: strain GA

Query Match 13.5%; Score 210; DB 2; Length 249;
Best Local Similarity 25.9%; Pred. No. 7.1e-06;
Matches 74; Conservative 33; Mismatches 93; Indels 86; Gaps 9;

OY 38 DTSRRCALGTRSRQGEVRFQYDESDYALYGGSSSEDEDEHEVP-----RTRRPVSGA 91
DB 3 DSERRKSSERRS-----LGTPSAVD--VSIAPRRSTKQRLNOD 42
OY 92 VLSGPPARAPPPAGSGAGRTPTTAPRAPRTQV-ATKAPAPAAETTRGRKSAOPES 150
DB 43 DLSKHGPFTHDP-----TQKYKSAKAVSEDSVSTTRGGFTNKP-- 80

QY 151 AALPDAPASTAPTAKTPAAGL-ARKLHSTAPNDPAPTPRVAGFNKRVCAAVGRLA 209
 C:Accession: S04713
 R:Cheung, A.K.
 Nucleic Acids Res. 17, 4637-4646, 1989
 A:Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies
 A:Reference number: S04713; MID:89315207
 A:Accession: S04713
 A:Molecule type: DNA
 A:Residues: 1-1460 <CHE>
 C:Superfamily: herpesvirus immediate-early protein IE175
 C:Keywords: DNA binding; early protein; transcription regulation

QY 210 AMHARMAAVALMMSRRPTDEDLNLGTTITVYCEGNL-----LQ 253
 DB 128 QYHAYGALALMRODPPRTNEELDAFSAVAVIKITIOEGNPLNGEAFETCARKLEESGLS 187

QY 254 RANELVNPVQDDAATATRG-----SRAASRPTERRAPARS 292
 DB 188 QGNENKSKSERTTKSERTRGEIEIKSPDPGSHRNRTATTS 233

RESULT 9
 QOBE3
 BHLF1 protein - human herpesvirus 4 (strain B95-8)
 C:Species: human herpesvirus 4, Epstein-Barr virus
 C:Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 23-Aug-1997
 C:Accession: A03742
 R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrall, B.G.
 Mol. Biol. Med. 1, 21-45, 1983
 A:Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus
 A:Reference number: A93065; MID:85055713
 A:Accession: A03742
 A:Molecule type: DNA
 A:Residues: 1-660 <BAN>
 R:Baer, R.; Bankier, A.T.; Blaglin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
 Nature 310, 207-211, 1984
 A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
 A:Contents: annotation; protein coding region
 C:Comment: The sequence contains four perfect repeats (residues 149-273, 274-398, 399-52
 C:Superfamily: human herpesvirus 4 BHLF1 protein

Query Match 10.3%; Score 161.5; DB 1; Length 660;
 Best Local Similarity 23.8%; Pred. No. 0.014;
 Matches 89; Conservative 21; Mismatches 133; Indels 131; Gaps 12;

QY 3 SRSVSGPREVPRDEEDLYTPSSGMASSPDPSTSRGALQTRSGEVRVQYDE 62
 DB 87 SRSRRTGPAE-----QADHAHSNPTGCGSPDPS-----KTRQAG----- 123

QY 63 SDYALYCGSSSEDD-----EHPVPTTRPVSGAVLSCGPAP----- 100
 DB 124 --YALGSGSGLSGRPRHAFQVQMSARNPGCPRTWRSSGQCHPRRPGAGQRPSP 181

QY 101 -----APPPA--GSGGAGRTPTTA-----PRAPRT 124
 DB 182 TGRPAAPGAPGTTPAAGPAGVAPGATPHRERGSGPADPAAARLPREDEPRLPD 241

QY 125 ORVATKAPAP-----AAETTRGKSAOPESALPDPAD-----ASTAPTRSKTPAOG 172
 DB 242 LAAAGKRPACPPPTRSAAAOQTHRRPCCPRSAKRNPGCCTRTWRKRSAGARGNRPPACQ 301

QY 173 ARKLHSTAPNDPAPTPRVAGFNKRVCAAVGRLAAMHARMAAVALMMSRRPTDEDL 232
 DB 302 RPSGPTGAPAPGAPCTPAAPGCGG--AAVSGATPHRERGSGADPPAAARLPRE 358

QY 233 NELLGTTITVYCEGNLQANELVNPVQDDA-----TATRRSAAASRPTER 285
 DB 359 QE-----PRLPDLLAAOQCPAGRPPTRSAGAAAOQTHRR 392

QY 286 PRAPARSRRPR 299
 DB 393 PRCPSARNPCCP 406

RESULT 10
 EDBE1F
 Immediate-early protein IE180 - suid herpesvirus 1 (strain Indiana-Funkhauser)
 C:Species: suid herpesvirus 1

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Feb-1997
 C:Accession: S04713
 R:Cheung, A.K.
 Nucleic Acids Res. 17, 4637-4646, 1989
 A:Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies
 A:Reference number: S04713; MID:89315207
 A:Accession: S04713
 A:Molecule type: DNA
 A:Residues: 1-1460 <CHE>
 C:Superfamily: herpesvirus immediate-early protein IE175
 C:Keywords: DNA binding; early protein; transcription regulation

Query Match 10.3%; Score 161; DB 1; Length 1460;
 Best Local Similarity 23.5%; Pred. No. 0.033;
 Matches 92; Conservative 24; Mismatches 127; Indels 148; Gaps 17;

QY 3 SRSVSGPREVPRDEEDLYTP-----SSGMASSPDPSTSRGA 44
 DB 42 SRRGSSG-----EDLLFGPGLFSDDAEAENAVLAAGATRRPRP-----SA 87

QY 45 LQTRSGEVRVQYDESDYALYCGSSSEDDHEPVRTTRPVSGAV-----LSGP 96
 DB 88 QOQRHARGSGEIVLDDDE-----EEDEPGSPAAGSVGLSRAPSTVTSSGP 138

QY 97 GPAPARPP-----PAGSGAGRTPTTAPAPRTQVATYAPAAAEETRG-- 142
 DB 139 GPAPAPGRRPRQNSQRRGPRPAAPGAPRRPRPPRRAPAPAPARRRGD 198

QY 143 -----RKSAQPE-----SAALDDAPASTPTSK-----T 167
 DB 199 PRGRTSRVSPRRRGIGRRHNSQRRGPRPAAPGAPRRPRPPRRAPAPARRRGD 256

QY 168 PAQGLARKLHSTAP-----NPDAPTPRVAGFNKRVCAAVGRLAAMHARMA 216
 DB 257 PAEGTAVVTTTSTASPLDPRPAARLDPAARREPRRLQPL-----QLQDHNHRR 310

QY 217 AVOILMDSRPTDEDLNLGTTITVYCEGNL-----LQANELVNPVQDDAAT 271
 DB 311 RAR-----RPRPRE-----GRGTRPRGRGAPLQRPRRRAGE-----GA 347

QY 272 ATRG---SAASRPTERRAPARSRRPR 299
 DB 348 LRKRGFSSSSSGSDSLSPARSPAPRAP 378

RESULT 11
 A45344
 Immediate-early protein - suid herpesvirus 1 (strain Kaplan)
 C:Species: suid herpesvirus 1
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
 C:Accession: A45344
 R:Vitek, C.; Kozmik, Z.; Paces, V.; Schlrm, S.; Schwytzer, M.
 Virology 179, 365-377, 1990
 A:Title: Pseudorabies virus immediate-early gene overlaps with an oppositely oriented
 A:Reference number: A45344; MID:91021039
 A:Accession: A45344
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1446 <VLG>
 A:Cross-references: GB:M34651; NID:q334070; PIDN:AAA47470.1; PID:q334071
 C:Superfamily: herpesvirus immediate-early protein IE175
 C:Keywords: DNA binding; early protein; transcription regulation

Query Match 9.8%; Score 153.5; DB 1; Length 1446;
 Best Local Similarity 25.1%; Pred. No. 0.091;
 Matches 93; Conservative 35; Mismatches 129; Indels 113; Gaps 18;

QY 3 SRSVSGPREVPRDEEDLYTP-----SSGMASSPDPSTSRGA 44
 DB 41 SRRGSSG-----EDLLFGPGLFSDDAEAENAVLAAGATRRPRP-----SA 86

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-839 <WH1>
A:Cross-references: GB:AE001904; GB:AE00513; NID:g6458129; PIDN:AAF10038.1; PID:g645814
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0458
A:Map position: 1
C:Superfamily: herpesvirus immediate-early protein IE110; RING finger homology

Query Match 9.4%; Score 146; DB 2; Length 839;
Best Local Similarity 22.3%; Pred. No. 0.15;

Matches 80; Conservative 35; Mismatches 104; Indels 140; Gaps 18;

QY 7 VKSGPREVPDEVEDLYTPSSGMASSPDSPDPT-----SRGALQTSRQGEVRFVQYDE 62
DB 207 VQAPPTPTP-----PQQAARPTPNAPQTPATQTPAQAQTPAQ----- 246
QY 63 SDYALYGGSSSEDEHPEVPTRRPVSGAVLSCGPAPARPPAGS----- 108
DB 247 -----APATQTPATP-APAAQRPAGAPSPAPAPAQA-NADAGSVPEATVPESTPA 297
QY 109 GGAGRTPTTAPR-----APRTQRYATKAPAPAAETTRGR---KSAOPESAA----- 152
DB 298 APSAQTPPTPTRETACTEASPAAPNSSAAPNBPASEPVAGPCTAASSPESASPVTVTP 357
QY 153 ---LPDAPAST-----APTRSS-----KTPAQGLARKLHFSTAPPNPDAPWTP 191
DB 358 RGETPPTAASAGTSPSAGRTVPAPAPSPASSEGASAKRTPGAG-----SQTPTPTATP--- 407
QY 192 RVAGFKRVFCAAVGRLAAMHARMAAVQIWMDSRPR---TDEDLNLGLGTTTIRVTVC 246
DB 408 -----IPATPAGRSSSGSAGTAA-----ARPNAAPAVSEDSVSGGLPR----- 447
QY 247 EGNLQIRANELVNPVDVDAATATRGKASRPTERRA--PAR-----SASRPR 297
DB 448 -----REDAPAESPVAAAPARGASSAPASAPAAVPSRAVPSGGSVSAPR 493

RESULT 15

B87254

Translation Initiation factor IF-2 [Imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: B87254

R:Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: B87254

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1037 <STC>

A:Cross-references: GB:AE005673; NID:g13421134; PIDN:AAK22030.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC0042

C:Superfamily: translation initiation factor IF-2; translation elongation factor Tu hom

Query Match 9.2%; Score 144; DB 2; Length 1037;
Best Local Similarity 24.2%; Pred. No. 0.24;

Matches 79; Conservative 31; Mismatches 104; Indels 112; Gaps 14;

QY 54 EVR---FVOTDESDVLY--GGSSSE--DDEHP-----EVPTRRPVSGAVLSG----- 95
DB 2 EVRPGFLLTWNERFFSVPPGGSTSERMSDENENGRPGRTPTLKRQGSVSGAVVKOS 61
QY 96 -----GPARAPPPAGSGAG----- 112
DB 62 FSHGRKTYVVTETKRTTAHAPASGNLAAPSSAERRHGEAPAPRPAPPGGGGAGGLSQ 121

QY 113 -----RTPTTAPRAPRTQRYATKA-----PAAPAAETTRGRKSAOPESAAP-----D 155
DB 122 EELRARGVVDAREAQARQVAAAEARARAAQEAQAEAAKAAAEERAAAAAPPPVQ 181
QY 156 APASTAPTRSKTPAQGLARKLHFSTAP-----PNPDAPWTPRVAGFKRVFCAAVGRLAAM 211
DB 182 APAPAPAPADVTPPPAPAPQ-----APRPVQAAPVAPASAPRQDAPQDTRAAAPGQ----- 231
QY 212 HARMAAVQIWMDSRPRPTDEDLNLGLGTTTIRVTVCSEGNLQIRANELVNPVDVDAAT 271
DB 232 -----TRTPEPSRDRDRDPS-----TTYTRPAPQGDPRFPNORA---PRD-----AN 271
QY 272 ATRGRSAASRPTERRPAPAPARSASRPR 297
DB 272 ANFGQRAPREGRDPRGPRPDGDRPQ 297

Search completed: August 28, 2002, 12:24:24
Job time: 233 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2002, 12:20:11 ; Search time 13.11 Seconds

(without alignments)
560.801 Million cell updates/sec

Title: US-09-522-278B-12

Perfect score: 1561

Sequence: 1 MTSRSVSKSGPREVPDEYE.....PTERRAPARSASRRPVE 301

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1561	100.0	301	US-08-303-861-21	Sequence 21, Appl
2	1561	100.0	301	US-09-011-073A-1	Sequence 1, Appl
3	1548	99.2	301	US-09-230-421-2	Sequence 2, Appl
4	1203.5	77.1	246	US-09-336-093-5	Sequence 5, Appl
5	573	36.7	144	US-09-420-421-3	Sequence 3, Appl
6	271.5	17.4	258	US-08-303-861-18	Sequence 18, Appl
7	271.5	17.4	258	US-08-303-861-19	Sequence 19, Appl
8	271.5	17.4	258	US-09-213-343-2	Sequence 2, Appl
9	225.5	14.4	302	US-08-303-861-20	Sequence 6, Appl
10	172.5	11.1	139	US-08-680-726A-66	Sequence 20, Appl
11	172.5	11.1	139	US-09-092-409-66	Sequence 66, Appl
12	169	10.8	34	US-09-011-073A-2	Sequence 6, Appl
13	166	10.6	32	US-09-230-421-14	Sequence 14, Appl
14	142.5	9.1	263	PCIT-US91-06532-2	Sequence 2, Appl
15	141	9.0	258	US-08-483-533-26	Sequence 26, Appl
16	141	9.0	258	US-09-283-471A-26	Sequence 26, Appl
17	141	9.0	264	US-08-483-533-40	Sequence 40, Appl
18	141	9.0	264	US-09-283-471A-40	Sequence 40, Appl
19	136.5	8.7	355	US-08-483-533-41	Sequence 41, Appl
20	136.5	8.7	355	US-09-283-471A-41	Sequence 41, Appl
21	136.5	8.7	355	PCIT-US91-06532-3	Sequence 3, Appl
22	131.5	8.4	661	US-08-795-868-14	Sequence 14, Appl
23	131.5	8.4	661	US-09-303-069-14	Sequence 14, Appl
24	130.5	8.4	591	US-09-082-737-2	Sequence 2, Appl
25	129.5	8.3	252	US-08-483-533-43	Sequence 43, Appl
26	129.5	8.3	252	US-09-283-471A-43	Sequence 43, Appl
27	128	8.2	882	US-09-413-814-78	Sequence 78, Appl

28	127.5	8.2	404	US-09-232-468A-8	Sequence 8, Appl
29	126.5	8.1	1298	US-08-690-473-2	Sequence 2, Appl
30	126.5	8.1	1298	US-09-259-821A-2	Sequence 2, Appl
31	126.5	8.1	1298	US-08-843-659-2	Sequence 2, Appl
32	122	7.8	265	US-09-199-637A-369	Sequence 369, App
33	120	7.7	1060	US-08-931-820-3	Sequence 3, Appl
34	120	7.7	1418	US-08-963-825-20	Sequence 20, Appl
35	120	7.7	1418	US-09-010-999-1	Sequence 1, Appl
36	120	7.7	1418	US-09-570-573-20	Sequence 20, Appl
37	120	7.7	1418	US-09-548-608-20	Sequence 20, Appl
38	119.5	7.7	169	US-08-483-533-28	Sequence 28, Appl
39	119.5	7.7	169	US-09-283-471A-28	Sequence 28, Appl
40	118	7.6	1426	US-09-136-574A-43	Sequence 43, Appl
41	118	7.6	1442	US-08-316-650-12	Sequence 12, Appl
42	118	7.6	1442	PCIT-US95-02251-12	Sequence 12, Appl
43	117	7.5	20	US-09-230-421-6	Sequence 6, Appl
44	116	7.4	507	US-08-860-635A-19	Sequence 19, Appl
45	116	7.4	507	US-09-281-476-19	Sequence 19, Appl

ALIGNMENTS

```
RESULT 1
US-08-303-861-21
; Sequence 21, Application US/08303861
; Patent No 6086902
; GENERAL INFORMATION:
; APPLICANT: ZAMB, TIMOTHY
; APPLICANT: LIANG, XIAOPING
; APPLICANT: BABIUK, LORNE A.
; TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE I
; TITLE OF INVENTION: VACCINES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,861
; FILING DATE: 09-SEP-1994
; CLASSIFICATION: A43
; ATTORNEY/AGENT INFORMATION:
; NAME: PARK, FREDIE K.
; REGISTRATION NUMBER: 35,636
; REFERENCE/DOCKET NUMBER: 29310-20020.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEEX: 706141
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-303-861-21

Query Match 100.0%; Score 1561; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 1.7e-127;
Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MTSRSVSKSGPREVPDEEDLYTPSSGMASSPDDTSRRGALQTRSGRGEVRFVQY 60
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Db 1 MTSRRSVKSGPREVPREDYEDLYTTPSSGMSASPDSPDTSRRGALOTRSRQGEVRFVQY 60
QY 61 DESDYALVGGSSSEDDHEPVPRTTRRVSGAVLSGPGPARAPPAGSGAGTPTTAPR 120
Db 61 DESDYALVGGSSSEDDHEPVPRTTRRVSGAVLSGPGPARAPPAGSGAGTPTTAPR 120
QY 121 APPTORVATKAPAAPAAETTRGRKSAQPEESALPDAPASTAPTRSKTPAOGCLARKLHFT 180
Db 121 APPTORVATKAPAAPAAETTRGRKSAQPEESALPDAPASTAPTRSKTPAOGCLARKLHFT 180
QY 181 APPNPDAPWTPRVAGFNRVFCAGVRLAAMHMAAVOLMDSRPTDEDLNELLGITTT 240
Db 181 APPNPDAPWTPRVAGFNRVFCAGVRLAAMHMAAVOLMDSRPTDEDLNELLGITTT 240
QY 241 IRVTVEGKNLQORANELVNDVVDVDDATATRGSAASRPTERRPARASASRPRPV 300
Db 241 IRVTVEGKNLQORANELVNDVVDVDDATATRGSAASRPTERRPARASASRPRPV 300
QY 301 E 301
Db 301 E 301

RESULT 2
US-09-011-073A-1
; Sequence 2 Application US/09011073A
; Patent No. 6184038
; GENERAL INFORMATION
; APPLICANT: OCHS et al.
; TITLE OF INVENTION: TRANSPORT PROTEINS AND THEIR USES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Klargust Sparkman Campbell Leigh &
; ADDRESS: Winston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204-2988
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 7.0 & ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,073A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/01831
; FILING DATE: JULY 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Earp, David J.
; REGISTRATION NUMBER: 41,401
; REFERENCE/DOCKET NUMBER: 5759-49294/DJE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-011-073A-1

Query Match 100.0%; Score 1561; DB 4; Length 301;
Best Local Similarity 100.0%; Pred. No. 1.7e-127;
Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSRRSVKSGPREVPREDYEDLYTTPSSGMSASPDSPDTSRRGALOTRSRQGEVRFVQY 60
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Db 61 DESDYALVGGSSSEDDHEPVPRTTRRVSGAVLSGPGPARAPPAGSGAGTPTTAPR 120
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Db 121 APPTORVATKAPAAPAAETTRGRKSAQPEESALPDAPASTAPTRSKTPAOGCLARKLHFT 180
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Db 181 APPNPDAPWTPRVAGFNRVFCAGVRLAAMHMAAVOLMDSRPTDEDLNELLGITTT 240
QY 241 IRVTVEGKNLQORANELVNDVVDVDDATATRGSAASRPTERRPARASASRPRPV 300
Db 241 IRVTVEGKNLQORANELVNDVVDVDDATATRGSAASRPTERRPARASASRPRPV 300
QY 301 E 301
Db 301 E 301

RESULT 3
US-09-230-421-2
; Sequence 2 Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL AGENTS AND ASSAYS
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 2
; LENGTH: 301
; TYPE: PRT
; ORGANISM: HERPESVIRUS TYPE 1
; US-09-230-421-2

Query Match 99.2%; Score 1548; DB 4; Length 301;
Best Local Similarity 99.3%; Pred. No. 2.3e-126;
Matches 299; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTSRRSVKSGPREVPREDYEDLYTTPSSGMSASPDSPDTSRRGALOTRSRQGEVRFVQY 60
Db 1 MTSRRSVKSGPREVPREDYEDLYTTPSSGMSASPDSPDTSRRGALOTRSRQGEVRFVQY 60
QY 61 DESDYALVGGSSSEDDHEPVPRTTRRVSGAVLSGPGPARAPPAGSGAGTPTTAPR 120
Db 61 DESDYALVGGSSSEDDHEPVPRTTRRVSGAVLSGPGPARAPPAGSGAGTPTTAPR 120
QY 121 APPTORVATKAPAAPAAETTRGRKSAQPEESALPDAPASTAPTRSKTPAOGCLARKLHFT 180
Db 121 APPTORVATKAPAAPAAETTRGRKSAQPEESALPDAPASTAPTRSKTPAOGCLARKLHFT 180
QY 181 APPNPDAPWTPRVAGFNRVFCAGVRLAAMHMAAVOLMDSRPTDEDLNELLGITTT 240
Db 181 APPNPDAPWTPRVAGFNRVFCAGVRLAAMHMAAVOLMDSRPTDEDLNELLGITTT 240
QY 241 IRVTVEGKNLQORANELVNDVVDVDDATATRGSAASRPTERRPARASASRPRPV 300
Db 241 IRVTVEGKNLQORANELVNDVVDVDDATATRGSAASRPTERRPARASASRPRPV 300
QY 301 E 301
Db 301 E 301

RESULT 4
US-09-336-093-5
; Sequence 5, Application US/09336093A
; Patient No. 6348185
; GENERAL INFORMATION:
; APPLICANT: Washington University School of Medicine
; TITLE OF INVENTION: MEMBRANE-PERMEANT PEPTIDE COMPLEXES FOR MEDICAL
; FILE OF INVENTION: IMAGING, DIAGNOSTICS, AND PHARMACEUTICAL THERAPY
; FILE REFERENCE: WSHU 2001
; CURRENT APPLICATION NUMBER: US/09/336,093A
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Herpes simplex virus VP22 protein
US-09-336-093-5

Query Match 77.1%; Score 1203.5; DB 4; Length 246;
Best Local Similarity 80.7%; Pred. No. 1e-96;
Matches 243; Conservative 0; Mismatches 3; Indels 55; Gaps 2;

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DB 1 MTSRSVSGPREVPDEDELYTPSSGMASSPDSPTSRGALOTRSGEVEFVOY 60
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DB 61 DESDYALYGSSSEDEDEHVEVPRTRRPSGAVLSGPGAPAPPPAGSGAGRTPTTAPR 120
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DB 181 APPNDAPWTPRVAGFNKRVCAVGRILAMHARMAAVOLMMSRPRTDEDLNLGLIT 240
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DB 241 IRVTVEGKNNLQANELNPNVDVDAATATGRSAASRPTERRAPARSRRPRPV 300
QY 301 E 301
DB 301 E 301
QY 246 E 246
DB 246 E 246

RESULT 5
US-09-230-421-3
; Sequence 7, Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL AGENTS AND ASSAYS
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
US-09-230-421-3

Query Match 36.7%; Score 573; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.7e-42;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 22 ASTAPTAKSTPAQGLARKLHSTAPNDPAPTPRVAGFNKRVCAVGRILAMHARMA 81
QY 218 VOLMDMSRPRTDEDLNLGLITTRVTVCEGKNNLQANELNPNVDV 267
DB 82 VOLMDMSRPRTDEDLNLGLITTRVTVCEGKNNLQANELNPNVDV 131

RESULT 6
US-08-303-861-18
; Sequence 18, Application US/08303861
; Patent No. 6086902
; GENERAL INFORMATION:
; APPLICANT: ZAMB, TIMOTHY
; APPLICANT: LIANG, XIAOPING
; APPLICANT: BABIUK, LORNE A.
; TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE I
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,861
; FILING DATE: 09-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PARK, FREDIE K.
; REGISTRATION NUMBER: 35,636
; REFERENCE/DOCKET NUMBER: 29310-20020, 20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 258 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-303-861-18

Query Match 17.4%; Score 271.5; DB 3; Length 258;
Best Local Similarity 31.2%; Pred. No. 4e-16;
Matches 81; Conservative 25; Mismatches 109; Indels 45; Gaps 8;

QY 61 DESDY-----ALVGGSSSEDEDEHVEVPRTRRPSGAVLSGPGP-----A 99
DB 10 DEDDYEDSLWVRENSLDYEGSDHYEELR-----AATSGPEBGRASVRACAS 62
QY 100 RAPPAGSG-----GAGRT---PTTAPRAPPTQVATKAPAAPA-----AETTRGRKSA 146
DB 63 AAAYGPAAAGRRRAAAGTTVAAPAAAPARRSSASRPPRAADPYLRATRTGSSGG 122
QY 147 QPESALPDAPASTAPTAKSTPAQGLARKLHSTAPNDPAPTPRVAGFNKRVCAV 206
DB 123 AGAVAVGP--PRRAPPGANAVASG--RPLAFSAAPKTPKAPWCGPTAYNRTICCAVA 178

OY 207 RLAAHARAQAALVMDMSRPTDEDNELLGITITVTCCEGKNNLORANELVNPVOD 266
DB 179 LVAEYARQAALVMDSDPKSNERLDRMLKSAIRILVCEGSGLLAANDILAARAQR 238
OY 267 VDAATATGRSAASRPTERR 286
DB 239 AARGSTSGESRLRGERARP 258

RESULT 7

US-08-303-861-19
; Sequence 19, Application US/08303861
; Patent No. 6086902
; GENERAL INFORMATION:
; APPLICANT: ZAMB, TIMOTHY
; APPLICANT: LIANG, XIAOPING
; APPLICANT: BABIUK, LORNE A.
; TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE I
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,861
; FILING DATE: 09-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PARK, FREDIE K.
; REGISTRATION NUMBER: 35,636
; REFERENCE/DOCKET NUMBER: 29310-20020.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 258 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-303-861-19

Query Match 17.4%; Score 271.5; DB 3; Length 258;
Best Local Similarity 31.2%; Pred. No. 4e-16;
Matches 81; Conservative 25; Mismatches 109; Indels 45; Gaps 8;

OY 61 DESDY-----ALYGGSSSEDEHPEVPTRRPVSGAVLGGP-----A 99
DB 10 DEDDYEDSLWRENSLYDESGSDHYVELR-----AATSGPEPGRASVRACAS 62
OY 100 RAPPAGSG-----GAGRT---PTTAPRAPRTQVATKAPAA-----AETTRGRKSA 146
DB 63 AAQVOPAAARGDRRAAAGTTVAAPAAAPARRSSSRASRPRAADPPVLRPATRGSSCG 122
OY 147 QPESALPDAPASTARTRSKTPAOGIARUKLHFTAPNPDAPTPRVAGFNKRVFCAAG 206
DB 123 AGAVAVGP--PRRAPPGANAASG--RPLAFSAARKTPKAPWCPTTHAVNRTIFCEAVA 178
OY 207 RLAAHARAQAALVMDMSRPTDEDNELLGITITVTCCEGKNNLORANELVNPVOD 266
DB 179 LVAEYARQAALVMDSDPKSNERLDRMLKSAIRILVCEGSGLLAANDILAARAQR 238

OY 267 VDAATATGRSAASRPTERR 286
DB 239 AARGSTSGESRLRGERARP 258

RESULT 8

US-09-213-343-2
; Sequence 2, Application US/09213343
; Patent No. 6316252
; GENERAL INFORMATION:
; APPLICANT: Harms, Jerome S.
; APPLICANT: Splitter, Gary A.
; TITLE OF INVENTION: Biotherapeutic Delivery System
; FILE REFERENCE: 960296.95364
; CURRENT APPLICATION NUMBER: US/09/213,343
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Bovine herpesvirus.1
; US-09-213-343-2

Query Match 17.4%; Score 271.5; DB 4; Length 258;
Best Local Similarity 31.2%; Pred. No. 4e-16;
Matches 81; Conservative 25; Mismatches 109; Indels 45; Gaps 8;

OY 61 DESDY-----ALYGGSSSEDEHPEVPTRRPVSGAVLGGP-----A 99
DB 10 DEDDYEDSLWRENSLYDESGSDHYVELR-----AATSGPEPGRASVRACAS 62
OY 100 RAPPAGSG-----GAGRT---PTTAPRAPRTQVATKAPAA-----AETTRGRKSA 146
DB 63 AAQVOPAAARGDRRAAAGTTVAAPAAAPARRSSSRASRPRAADPPVLRPATRGSSCG 122
OY 147 QPESALPDAPASTARTRSKTPAOGIARUKLHFTAPNPDAPTPRVAGFNKRVFCAAG 206
DB 123 AGAVAVGP--PRRAPPGANAASG--RPLAFSAARKTPKAPWCPTTHAVNRTIFCEAVA 178
OY 207 RLAAHARAQAALVMDMSRPTDEDNELLGITITVTCCEGKNNLORANELVNPVOD 266
DB 179 LVAEYARQAALVMDSDPKSNERLDRMLKSAIRILVCEGSGLLAANDILAARAQR 238
OY 267 VDAATATGRSAASRPTERR 286
DB 239 AARGSTSGESRLRGERARP 258

RESULT 9

US-08-303-861-20
; Sequence 20, Application US/08303861
; Patent No. 6086902
; GENERAL INFORMATION:
; APPLICANT: ZAMB, TIMOTHY
; APPLICANT: LIANG, XIAOPING
; APPLICANT: BABIUK, LORNE A.
; TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE I
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30